

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model.

Run on: November 15, 2005, 23:53:58 ; Search time 31202 Seconds
(without alignments)
11774.484 Million cell updates/sec

Title: US-10-717-580-11
Perfect score: 7582
Sequence: 1 caacaatcggtataaacc.....tattaatctgtcactgtc 7582

Scoring table: IDENTITY NUC
Gapop 10.0 ; Gapext 1.0

Searched: 4708233 seqs, 24227607955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_ba.*
- 2: gb_hg.*
- 3: gb_in.*
- 4: gb_on.*
- 5: gb_ov.*
- 6: gb_pat.*
- 7: gb_ph.*
- 8: gb_pl.*
- 9: gb_pr.*
- 10: gb_ro.*
- 11: gb_sts.*
- 12: gb_sy.*
- 13: gb_un.*
- 14: gb_vi.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	7489.6	98.8	7582	6	BD196245	BD196245 Endogenet
2	7489.6	98.8	7582	6	BD267487	BD267487 Endogenet
3	7489.6	98.8	7582	6	AX000966	AX000966 Sequence
4	7489.6	98.8	7582	6	AX027480	AX027480 Sequence
5	6448	85.0	10222	9	AY101582	AY101582 Homo sapi
6	6448	85.0	10222	9	AY101585	AY101585 Homo sapi
7	6448	85.0	56093	9	HSAC000064	AX329572 Sequence
8	6448	85.0	149194	9	AC007566	AC007566 Homo sapi
9	6448	85.0	10222	9	AY101583	AY101583 Homo sapi
10	6446.4	84.9	10222	6	BD221808	BD221808 Nucleic s
11	6440	84.9	10499	6	AX007980	AX007980 Sequence
12	6436	84.9	10499	6	AY101586	AY101586 Pan trogl
13	6346.4	83.7	10229	9	AY101587	AY101587 Pan trogl
14	6344.8	83.7	10229	9	AC145964	AC145964 Pan trogl
15	6344.8	83.7	184675	9	AY101588	AY101588 Gorilla g
16	6269.6	82.7	10230	9	AY101589	AY101589 Gorilla g
17	6269.6	82.7	10230	9	AY101590	AY101590 Pongo pyg
18	6037.8	79.6	10122	9		

20	6025.8	79.5	10124	9	AY101591	AY101591 Pongo pyg
21	5956.8	78.6	10246	9	AY101593	AY101593 Hylobates
22	5950.4	78.5	10248	9	AY101592	AY101592 Hylobates
c	5824.2	76.8	158033	9	AC018926	AC018926 Homo sapi
23	5492	72.4	105989	9	AC008121	AC008121 Homo sapi
24	5492	72.4	110000	2	AC009727_2	Continuation (3 of
c	4755.6	62.7	187321	2	AC092510	AC092510 Papio anu
25	4302.2	56.7	114621	2	AC005187	AC005187 Homo sapi
c	4295.8	56.7	46575	2	AC080036	AC080036 Homo sapi
26	3944.6	52.0	183680	9	AL592310	AL592310 Human DNA
c	3779.8	49.9	73070	9	AC098859	AC098859 Homo sapi
27	3731.6	49.2	173788	9	AL590143	AL590143 Human DNA
c	3731.6	49.2	185540	9	AC022555	AC022555 Homo sapi
28	3716.6	49.0	160883	2	AL158814	AL158814 Homo sapi
c	3537.2	46.7	137947	9	HS4514	AL023551 Human DNA
29	3442.8	45.4	205035	9	CNS00005	AL049870 Human chr
c	3438.2	45.3	101846	9	HS197L1	AL031390 Human DNA
30	3420.6	45.1	68693	9	AC108746	AC139260 Homo sapi
c	3367.4	44.4	118312	9	AC055713	AC108746 Homo sapi
31	3367.4	44.4	197549	2	AC145423	AC145423 Homo sapi
c	3300.6	43.5	169250	9	AP002812	AP002812 Homo sapi
32	3290.2	43.4	134412	2	AP002377	AP002377 Homo sapi

ALIGNMENTS

RESULT 1
BD196245
LOCUS BD196245 7582 bp DNA linear PAT 17-JUL-2003
DEFINITION Endogenetic retroviral sequences, associated with autoimmune diseases and/or with pregnancy disorders.
ACCESSION BD196245
VERSION BD196245.1 GI:33006015
KEYWORDS JP 2002512530-A/11.
SOURCE unclassified
ORGANISM unclassified
REFERENCE 1 (bases 1 to 7582)
AUTHORS Beseme, F., Blond, J.L., Bouton, O., Mandrand, B. and Mallet, F.
TITLE Endogenetic retroviral sequences, associated with autoimmune diseases and/or with pregnancy disorders
JOURNAL Patent: JP 2002512530-A 11 23-APR-2002;
COMMENT BIO MERIEUX
OS Unidentified
PN JP 2002512530-A/11
PD 23-APR-2002
PF 06-JUL-1998 JP 1999508244
PR 07-JUL-1997 FR 97/08815
PI FREDERIC BESEME, JEAN LUC BLOND, OLIVIER BOUTON, BERNARD MANDRAND.
PI FRANCIS WALLEY
PC C12N15/48, C07K14/15, C12Q1/68, C07K16/10, G01N33/569 CC
Strandedness: Single;
CC Topology: Linear;
CC Endogenetic retroviral sequences, associated with autoimmune diseases
CC and/or with pregnancy disorders
FH Key Location/Qualifiers
FT source 1. 7582
Location/Qualifiers
1. 7582
/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"

FEATURES
source

ORIGIN

Query Match

98.8%; Score 7489.6; DB 6; Length 7582;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 7582; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	CAACAAATCGGGATATAAACCCAGGCAATTCGAGCTGCAACAGCAGCCCCCTTTGGGTCC	60
DB	1	CAACAAATCGGGATATAAACCCAGGCAATTCGAGCTGCAACAGCAGCCCCCTTTGGGTCC	60
QY	61	CTTCCCTTTGTATGGGAGCTGTTTTCATGCTATTTCACTCTATTAATCTTGCAACTGCA	120
DB	61	CTTCCCTTTGTATGGGAGCTGTTTTCATGCTATTTCACTCTATTAATCTTGCAACTGCA	120
QY	121	CTCTTCTGTGTCATGTTTCTTAAGGCTCGAGCTGAGCTTTTGTCTCAACGTCACCACTGC	180
DB	121	CTCTTCTGTGTCATGTTTCTTAAGGCTCGAGCTGAGCTTTTGTCTCAACGTCACCACTGC	180
QY	181	TGTTTGGCAACCCGACACCTGCGCTGACTCCCATCTGCTCTGGAATCTGCAAGGTGTC	240
DB	181	TGTTTGGCAACCCGACACCTGCGCTGACTCCCATCTGCTCTGGAATCTGCAAGGTGTC	240
QY	241	CGCTGTGCTCCTGATCCAGCGAGCGCCCATTCGCGCTCCCAATTTGGGCTTAAAGGCTTGC	300
DB	241	CGCTGTGCTCCTGATCCAGCGAGCGCCCATTCGCGCTCCCAATTTGGGCTTAAAGGCTTGC	300
QY	301	CATTGTNCTGCAAGGCTTAAGTGCCTGGGTTGTTCTAATTTGAGCTGAACTANTCACT	360
DB	301	CATTGTNCTGCAAGGCTTAAGTGCCTGGGTTGTTCTAATTTGAGCTGAACTANTCACT	360
QY	361	GGGTTCCATGGTCTCTTCTGTGACCCAGGCTTCTAATAKAACTAATCACTTACCACA	420
DB	361	GGGTTCCATGGTCTCTTCTGTGACCCAGGCTTCTAATAKAACTAATCACTTACCACA	420
QY	421	TGGCCCAAGATTCATTTCTTGGAAATCGTGAGSCAAACGAACTCCAGGTACAGAAATAC	480
DB	421	TGGCCCAAGATTCATTTCTTGGAAATCGTGAGSCAAACGAACTCCAGGTACAGAAATAC	480
QY	481	GARGCTTGGCACCATCTTGGAAAGCGCTGCTACCTTGGAAAGTGGTTTCAACCAATC	540
DB	481	GARGCTTGGCACCATCTTGGAAAGCGCTGCTACCTTGGAAAGTGGTTTCAACCAATC	540
QY	541	TTGGGAGCTCTGTGAGCAAGGACCCCGGTACATTTTGGCBACCAACGAGCATCC	600
DB	541	TTGGGAGCTCTGTGAGCAAGGACCCCGGTACATTTTGGCBACCAACGAGCATCC	600
QY	601	MAAGTCAATGGAAACGTTCCCGCAAGACAAACGCGCTTAAGAGTATTTCTGGARAAT	660
DB	601	MAAGTCAATGGAAACGTTCCCGCAAGACAAACGCGCTTAAGAGTATTTCTGGARAAT	660
QY	661	TGGGAMCAATTTTGACCCCTCAGACACTAAGAAAGAAACGACTTATTTCTGCAAGTCC	720
DB	661	TGGGAMCAATTTTGACCCCTCAGACACTAAGAAAGAAACGACTTATTTCTGCAAGTCC	720
QY	721	GCTTGGCACTCTGAGGGAAGTATTAATTAATACCATCTTACAGCTAGACATCTTTTG	780
DB	721	GCTTGGCACTCTGAGGGAAGTATTAATTAATACCATCTTACAGCTAGACATCTTTTG	780
QY	781	TAGAAAGGCAATGAGTGAAGTGCATTAAGTACAAACCTTTCTTTTCAATTAAGAGACAA	840
DB	781	TAGAAAGGCAATGAGTGAAGTGCATTAAGTACAAACCTTTCTTTTCAATTAAGAGACAA	840
QY	841	CTCACAAATATGTAAAGTGTGATTTATGCCCTTACAGGAAGCTTTCAGAGTCTACCTCC	900
DB	841	CTCACAAATATGTAAAGTGTGATTTATGCCCTTACAGGAAGCTTTCAGAGTCTACCTCC	900
QY	901	CTATCCAGCATCCCGACTCTTCCCGCAATTAAGGACCCCGCTTCAACCCAAATGG	960
DB	901	CTATCCAGCATCCCGACTCTTCCCGCAATTAAGGACCCCGCTTCAACCCAAATGG	960
QY	961	TCCAAAGGAGTAGACAAAGGGTAAACAGTGAACCAAGAGTGCCTATTTCCCAAT	1020
DB	961	TCCAAAGGAGTAGACAAAGGGTAAACAGTGAACCAAGAGTGCCTATTTCCCAAT	1020
QY	1021	TATGACCCCTCCCAAGCAGTGGGAGGAGAAATTCGGCCACGACAGTGCATGTGCT	1080
DB	1021	TATGACCCCTCCCAAGCAGTGGGAGGAGAAATTCGGCCACGACAGTGCATGTGCT	1080

DB	1021	TATGACCCCTCCCAAGCAGTGGGAGGAGAAATTCGGCCACGACAGTGCATGTGCT	1080
QY	1081	TTTTTCTCCAGACTTAAAGCAAAATAAAACAGACTTAGGTAAATTTCTCAGATAATCCT	1140
DB	1081	TTTTTCTCCAGACTTAAAGCAAAATAAAACAGACTTAGGTAAATTTCTCAGATAATCCT	1140
QY	1141	GATGGCTATTTGRTGTTTTTACAGGGTTAGGACAAATTTCTTGATCTGACATGGAGAT	1200
DB	1141	GATGGCTATTTGRTGTTTTTACAGGGTTAGGACAAATTTCTTGATCTGACATGGAGAT	1200
QY	1201	ATATATGTCATCTGCTAAATCAGACACTAAACCCCAATAGAGAGAGTGCACCAATACCTGC	1260
DB	1201	ATATATGTCATCTGCTAAATCAGACACTAAACCCCAATAGAGAGAGTGCACCAATACCTGC	1260
QY	1261	AGCTTGAGGTTTTGGCGATCTCTGCTATCTCAGTCAGTCAATGGATANGGATGACAAACA	1320
DB	1261	AGCTTGAGGTTTTGGCGATCTCTGCTATCTCAGTCAGTCAATGGATANGGATGACAAACA	1320
QY	1321	GAGGAAAGANAATGATTTCCCAAGGCCAGCAGCAGTTCCTCAGTCTASACCTCATTTG	1380
DB	1321	GAGGAAAGANAATGATTTCCCAAGGCCAGCAGCAGTTCCTCAGTCTASACCTCATTTG	1380
QY	1381	GGGACACAGAAATCAGTAAATCAGTGGAGATTTGCTGTCAGACATTTGCTAACTTGCTGC	1440
DB	1381	GGGACACAGAAATCAGTAAATCAGTGGAGATTTGCTGTCAGACATTTGCTAACTTGCTGC	1440
QY	1441	TASAGGACTTAAGGAAACTASAGAAAGAAATCTAYGAAATTAATCTCAATGATGTCCACATA	1500
DB	1441	TASAGGACTTAAGGAAACTASAGAAAGAAATCTAYGAAATTAATCTCAATGATGTCCACATA	1500
QY	1501	ACACAGGGGAGGGAAGAAATCTCTACTGCTTTCTGAGAGACTAAGGGAGGCAITGAG	1560
DB	1501	ACACAGGGGAGGGAAGAAATCTCTACTGCTTTCTGAGAGACTAAGGGAGGCAITGAG	1560
QY	1561	GAGCGTGCCTCTCTGTCACTGACTCTTCTGAGGCCAACTAATCTTAAGCGTAACTT	1620
DB	1561	GAGCGTGCCTCTCTGTCACTGACTCTTCTGAGGCCAACTAATCTTAAGCGTAACTT	1620
QY	1621	TATCACTCAGTGCAGTGCAGACATTAAGAAAGAACTTCAAAAGTCTCGCTAGGCCGGAG	1680
DB	1621	TATCACTCAGTGCAGTGCAGACATTAAGAAAGAACTTCAAAAGTCTCGCTAGGCCGGAG	1680
QY	1681	CAAAAATTAGAAACCTTATTTGAACTTTGGCAACTTTGGAAGTCTGAGATCAGGAG	1740
DB	1681	CAAAAATTAGAAACCTTATTTGAACTTTGGCAACTTTGGAAGTCTGAGATCAGGAG	1740
QY	1741	GAGCAGCGGACAGACAAACGGGATTAAGAAAGGCAACCGCTTTAGTCAATGACCT	1800
DB	1741	GAGCAGCGGACAGACAAACGGGATTAAGAAAGGCAACCGCTTTAGTCAATGACCT	1800
QY	1801	CAGGCAAGTGGACTTTTGGAGGCTCTGAAAAGGGAAGCTGGGCAAAATTTGAATGCTTAA	1860
DB	1801	CAGGCAAGTGGACTTTTGGAGGCTCTGAAAAGGGAAGCTGGGCAAAATTTGAATGCTTAA	1860
QY	1861	TAGGGCTTCTTCCAGTGGGTCTACAAGGACACTTTTAAAAAGATTTGTCAGATGAGAG	1920
DB	1861	TAGGGCTTCTTCCAGTGGGTCTACAAGGACACTTTTAAAAAGATTTGTCAGATGAGAG	1920
QY	1921	TAAAGCCGCTTCTGCTCAATGCCCTTATTTCAAGGGAATCACTGGAGGCCCACTGCC	1980
DB	1921	TAAAGCCGCTTCTGCTCAATGCCCTTATTTCAAGGGAATCACTGGAGGCCCACTGCC	1980
QY	1981	CAGGGACAAAGGTCTTTTGAATCAGAACCACTAACACAGATGATCAGCAGCAGGACTG	2040
DB	1981	CAGGGACAAAGGTCTTTTGAATCAGAACCACTAACACAGATGATCAGCAGCAGGACTG	2040
QY	2041	AGGGTCTTGGGCAAGCGCCATCCCATGTCATCCCTCACAGAGCCCTGGGTATGCTT	2100
DB	2041	AGGGTCTTGGGCAAGCGCCATCCCATGTCATCCCTCACAGAGCCCTGGGTATGCTT	2100
QY	2101	GACCAATGAGGCGCAGGAGGTTGCTCTCTGGACACTGGTGGCTCTTCTTAGCTTACT	2160
DB	2101	GACCAATGAGGCGCAGGAGGTTGCTCTCTGGACACTGGTGGCTCTTCTTAGCTTACT	2160

QY	2161	CTTCTGTCCGGCAAACTGTCCTCCAGATCTGTCACTATTCTCGAGGGGTCONTAAGACG	2220
Db	2161	CTTCTGTCCGGCAAACTGTCCTCCAGATCTGTCACTATTCTCGAGGGGTCONTAAGACG	2220
QY	2221	GGCAGTCACTAGATATCTTTTCCAGCCTAAAGTATGAATGAGGAGCTTTATTTCTTT	2280
Db	2221	GGCAGTCACTAGATATCTTTTCCAGCCTAAAGTATGAATGAGGAGCTTTATTTCTTT	2280
QY	2281	TCAATGCTTTTCTTAATATGCTTGAAGCCCACTACCTTGTGAGGAGAGACATCTTA	2340
Db	2281	TCAATGCTTTTCTTAATATGCTTGAAGCCCACTACCTTGTGAGGAGAGACATCTTA	2340
QY	2341	GCAAAAGCAGGGGCCATTATACACCTGAACATAGGAGAGGAACACCCGTTTGTGTGCC	2400
Db	2341	GCAAAAGCAGGGGCCATTATACACCTGAACATAGGAGAGGAACACCCGTTTGTGTGCC	2400
QY	2401	CTGTCTTGAGGAAGGAATTAATCTGAAAGTCTGGGCAACAGAGGACAATATGGACGAGC	2460
Db	2401	CTGTCTTGAGGAAGGAATTAATCTGAAAGTCTGGGCAACAGAGGACAATATGGACGAGC	2460
QY	2461	CAAGAATGCCCGTCTGTTTCAAGTTAAACTAAAGGATTCACCTTCCCTTCCCTACCAA	2520
Db	2461	CAAGAATGCCCGTCTGTTTCAAGTTAAACTAAAGGATTCACCTTCCCTTCCCTACCAA	2520
QY	2521	GGCAGTACCCCTCAGACCCAGGCCCAACAGGATTCCAAAGATTTGTTAAGGACTTAA	2580
Db	2521	GGCAGTACCCCTCAGACCCAGGCCCAACAGGATTCCAAAGATTTGTTAAGGACTTAA	2580
QY	2581	AAGCCCAAGCTTAGTAAACCATGCACTAATCCCTGCAAGTAACTCCGTTAGTGGATTGAG	2640
Db	2581	AAGCCCAAGCTTAGTAAACCATGCACTAATCCCTGCAAGTAACTCCGTTAGTGGATTGAG	2640
QY	2641	GAGGCACAGAACCCAGTGGAGGAGGTTAGTGCAGATCTCAGAGTTATCAATGG	2700
Db	2641	GAGGCACAGAACCCAGTGGAGGAGGTTAGTGCAGATCTCAGAGTTATCAATGG	2700
QY	2701	AGGCCGTTGTCCTTTTATACCCAGCTGTACTAGCCCTTATCTGTGMYTTCCCAAAATAC	2760
Db	2701	AGGCCGTTGTCCTTTTATACCCAGCTGTACTAGCCCTTATCTGTGMYTTCCCAAAATAC	2760
QY	2761	CAGAGGAAGCAGAGTGGTTTAACTCTGGACCTTMAAGATCCCTTCTGATCCCTG	2820
Db	2761	CAGAGGAAGCAGAGTGGTTTAACTCTGGACCTTMAAGATCCCTTCTGATCCCTG	2820
QY	2821	TACATCTGACTCTCAATCTTGTGTTGCTTTGAAAGATCTTCAAAACCCARCATCTCAAC	2880
Db	2821	TACATCTGACTCTCAATCTTGTGTTGCTTTGAAAGATCTTCAAAACCCARCATCTCAAC	2880
QY	2881	TCACCTGGACTRTTTTATACCCAGGGTTTCAGGGATAGYCCCCATCTATTGSCCAGGCAT	2940
Db	2881	TCACCTGGACTRTTTTATACCCAGGGTTTCAGGGATAGYCCCCATCTATTGSCCAGGCAT	2940
QY	2941	TAGCCCAAGACTTGAGYCAATYMTCACTACCTGGACCTTGTGCTTCRGTAKGTGGATG	3000
Db	2941	TAGCCCAAGACTTGAGYCAATYMTCACTACCTGGACCTTGTGCTTCRGTAKGTGGATG	3000
QY	3001	ATTTACTTTTGGYCCYRTTCAGAAAACCTTGTGCCATCAAGCCACCCAGCRCTCTTMA	3060
Db	3001	ATTTACTTTTGGYCCYRTTCAGAAAACCTTGTGCCATCAAGCCACCCAGCRCTCTTMA	3060
QY	3061	ATTTCTCGYACCTGTGGCTACAGGTTTCCAAACARSARGCTCARTCTGCTCACAGC	3120
Db	3061	ATTTCTCGYACCTGTGGCTACAGGTTTCCAAACARSARGCTCARTCTGCTCACAGC	3120
QY	3121	AGGTTAAATACTTAGGCTTAARATTTATCAAGGCACCAAGGCCCTCAGTGAGGAAYRYA	3180
Db	3121	AGGTTAAATACTTAGGCTTAARATTTATCAAGGCACCAAGGCCCTCAGTGAGGAAYRYA	3180
QY	3181	TCCAGCCTATCTGCTTATCTCATCTATCYCAAAACCCCTAAAGCAATTAAGGRRTTCTTTG	3240
Db	3181	TCCAGCCTATCTGCTTATCTCATCTATCYCAAAACCCCTAAAGCAATTAAGGRRTTCTTTG	3240
QY	3241	GCRTAAYAGGYTTCTGCCGAATATGGAATTTCCCCAGGTWTGGCBAAATAGCCAGGYCATTA	3300
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QY	3301	WATACASTAATTAAGGAAACTCAGAAAGCCAATACCATTATTARTAAAGATGGAAMCTGAA	3360
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QY	3361	GYMRAAGTGGCTTTCCAGGCCCTTAAAGAGGCCCTTAAACCCCAAGYCCCAAGTGTAAAGYT	3420
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QY	3421	TGCCAACRGGGCAAGACTTTTSTTYATAVRTCACAGAAAACACAGRAAYAGCTCTRGGA	3480
Db	3421	TGCCAACRGGGCAAGACTTTTSTTYATAVRTCACAGAAAACACAGRAAYAGCTCTRGGA	3480
QY	3481	GTCTTACACAGRTCCRAGGGAYGAGCTTGCACACCVRTGGCRYACCTGASTAAGGAAAYT	3540
Db	3481	GTCTTACACAGRTCCRAGGGAYGAGCTTGCACACCVRTGGCRYACCTGASTAAGGAAAYT	3540
QY	3541	GATGTAGTGGCAAGGGTTGRCYTCATTGTTTAYGGGTAGTGGTGGCAGTACGAGTYKTA	3600
Db	3541	GATGTAGTGGCAAGGGTTGRCYTCATTGTTTAYGGGTAGTGGTGGCAGTACGAGTYKTA	3600
QY	3601	GTATCTGAAGCAGTTTAAATAATACAGGGRAGAGATCTTACTGTGTGGACATCTCATGAK	3660
Db	3601	GTATCTGAAGCAGTTTAAATAATACAGGGRAGAGATCTTACTGTGTGGACATCTCATGAK	3660
QY	3661	GTGAAYRGCATACTCACTGTCTAAAGGAGACTTGTGGCTGTGAGACAACVGTGTTACTTAA	3720
Db	3661	GTGAAYRGCATACTCACTGTCTAAAGGAGACTTGTGGCTGTGAGACAACVGTGTTACTTAA	3720
QY	3721	TRTCAGGCTCTATTACTTGAAGGCGCAGTGTGCRACCTGTGCACTTGTGCAACTCTTAAC	3780
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QY	3781	CCAGYCNCAATTTCTTCCAGACAATGAAGAAAGATARAAYATACTGTCTCAACAAATAAT	3840
Db	3781	CCAGYCNCAATTTCTTCCAGACAATGAAGAAAGATARAAYATACTGTCTCAACAAATAAT	3840
QY	3841	TCTCAAACTATGCCACTTCGAGGGGACCTTGTAGAGTTTCCYTTGACTGATCCYACCTT	3900
Db	3841	TCTCAAACTATGCCACTTCGAGGGGACCTTGTAGAGTTTCCYTTGACTGATCCYACCTT	3900
QY	3901	CAACTGTATATGATGAGGAGTCTCTTTGTAGAAAAGGACTTCGAAAAGYGGGGTATGC	3960
Db	3901	CAACTGTATATGATGAGGAGTCTCTTTGTAGAAAAGGACTTCGAAAAGYGGGGTATGC	3960
QY	3961	AGTGTGATGATATGGAATAYTTGAAAGTAATCCCTCACTCCAGGAACTAGTGTCTYA	4020
Db	3961	AGTGTGATGATATGGAATAYTTGAAAGTAATCCCTCACTCCAGGAACTAGTGTCTYA	4020
QY	4021	GCTRGCAAGAACTAATAGCCYTCAYTKGGGCACTAGAAATTAGGAGAAAGGAGGAAA	4080
Db	4021	GCTRGCAAGAACTAATAGCCYTCAYTKGGGCACTAGAAATTAGGAGAAAGGAGGAAA	4080
QY	4081	TATATATACAGACTCTTARTATGCTYACCTAGTCNTCCATGCCCATATGATGATGATG	4140
Db	4081	TATATATACAGACTCTTARTATGCTYACCTAGTCNTCCATGCCCATATGATGATGATG	4140
QY	4141	AGAAAGGGAATTCCTTAATCTTCYAGRGAAACCTTATCMAACATCAGGAAAGCATTAGGAR	4200
Db	4141	AGAAAGGGAATTCCTTAATCTTCYAGRGAAACCTTATCMAACATCAGGAAAGCATTAGGAR	4200
QY	4201	ATTATTAATGCGWGTACAGAAAACCTTAGAGGTGGMAGTCTTACACTGCGGGGTCACTCA	4260
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QY	4261	NAAGGAAAGGAAATASAGGAAATAGCAAGCAATATTAAGGCAAGGAGGAGC	4320
Db	4261	NAAGGAAAGGAAATASAGGAAATAGCAAGCAATATTAAGGCAAGGAGGAGC	4320
QY	4321	TGCAGGAGGAGCCCTCCATCTAGAAATGCTTATTAATAAATCCCTTAGTATAGGGTAATCC	4380

Db 4321 TGCAAGCGCAGGACCCCTCCATTAGAAATGCTTATTAACCTTCCCTTAGTATAGGGTAATCC 4380
Qy |||||
Db 4381 CTTCCGGGAAACCAAGCCCAAGTACTCAGCAGAGGAAACAGAAATGGGGACCTCAGAGG 4440
Qy |||||
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Qy |||||
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Qy |||||
Db 4441 CAGTTTTCTCCCTCGGAGCGGTTAGCCACTGAAGAGGGGAAATACTTTTGGCTGCAAC 4500
Qy |||||
Db 4501 TATCCAAATGGAATAATCTTAACCCCTTCAATCAACCTTTCACTTAGGCAATCAGTAGCAC 4560
Qy |||||
Db 4501 TATCCAAATGGAATAATCTTAACCCCTTCAATCAACCTTTCACTTAGGCAATCAGTAGCAC 4560
Qy |||||
Db 4561 CCATCARATGCGCAAAATCATTTTACTGACACAGGCGCTTTTCAAAACTATCAAGCARAT 4620
Qy |||||
Db 4561 CCATCARATGCGCAAAATCATTTTACTGACACAGGCGCTTTTCAAAACTATCAAGCARAT 4620
Qy |||||
Db 4621 AKTCAGGCGCTGTGAATGTGCCARARAAATAATCCCCTGCTTATGCGCAAGCTCCTTC 4680
Qy |||||
Db 4621 AKTCAGGCGCTGTGAATGTGCCARARAAATAATCCCCTGCTTATGCGCAAGCTCCTTC 4680
Qy |||||
Db 4681 AGGARAACAARAACAGGCGCAATTAACCTGRRARAARCTGGCAACTGATTTTACCCACAAG 4740
Qy |||||
Db 4681 AGGARAACAARAACAGGCGCAATTAACCTGRRARAARCTGGCAACTGATTTTACCCACAAG 4740
Qy |||||
Db 4741 CCCAAACCTCAGGGATTCAGTACTACTAGTCTGGGTARATCTTTTCAAGGGTTGGCA 4800
Qy |||||
Db 4741 CCCAAACCTCAGGGATTCAGTACTACTAGTCTGGGTARATCTTTTCAAGGGTTGGCA 4800
Qy |||||
Db 4801 RAGGCGCTTCCCTGTAGGACAGAAAAGGCCCAAGAGGTAAATAAGGCACCTAGTTTCATGAA 4860
Qy |||||
Db 4801 RAGGCGCTTCCCTGTAGGACAGAAAAGGCCCAAGAGGTAAATAAGGCACCTAGTTTCATGAA 4860
Qy |||||
Db 4861 ATAATTCAGATTCGGAATTCGCCAGGCTTACAGAGTGACAAATGATGAACTCAAGAGGACATCTA 5040
Qy |||||
Db 4861 ATAATTCAGATTCGGAATTCGCCAGGCTTACAGAGTGACAAATGATGAACTCAAGAGGACATCTA 5040
Qy |||||
Db 4921 GCCACAGTAACCCAGGAGTATCCAGCGGTAGGTATAGATACATCTACTACCTGCGCC 4980
Qy |||||
Db 4921 GCCACAGTAACCCAGGAGTATCCAGCGGTAGGTATAGATACATCTACTACCTGCGCC 4980
Qy |||||
Db 4981 TGAAGGCCACAGTCTCCTCAGGGAAGTCTGAGAAAATGAATGAAATCAAGAGGACATCTA 5040
Qy |||||
Db 4981 TGAAGGCCACAGTCTCCTCAGGGAAGTCTGAGAAAATGAATGAAATCAAGAGGACATCTA 5040
Qy |||||
Db 5041 AAAAAGCAAAACCCAGGAAAACCCACCTCACATGGCTGTCTGTGGCTATAGCCCTTAAA 5100
Qy |||||
Db 5041 AAAAAGCAAAACCCAGGAAAACCCACCTCACATGGCTGTCTGTGGCTATAGCCCTTAAA 5100
Qy |||||
Db 5101 AGAATCTGCAACTTTCCCAAAAGCAGGACTTAGCCCATACGAAATGCTGTAGGAAG 5160
Qy |||||
Db 5101 AGAATCTGCAACTTTCCCAAAAGCAGGACTTAGCCCATACGAAATGCTGTAGGAAG 5160
Qy |||||
Db 5161 CCCTTCATAACCAATGACCTTGTCTTGACCCCAAGACGCGCAACTTAGTTGCGACATCA 5220
Qy |||||
Db 5161 CCCTTCATAACCAATGACCTTGTCTTGACCCCAAGACGCGCAACTTAGTTGCGACATCA 5220
Qy |||||
Db 5221 CCTCTTAGCCAAATATCAACAGTTCTTAAACATTTACAGGAAACCTATCCCTGAGAAG 5280
Qy |||||
Db 5221 CCTCTTAGCCAAATATCAACAGTTCTTAAACATTTACAGGAAACCTATCCCTGAGAAG 5280
Qy |||||
Db 5281 AGGAAAAGAACATTTCCACCCWGTGACATGGTATTAGTCAAGTCCCTTCCTTAAT 5340
Qy |||||
Db 5281 AGGAAAAGAACATTTCCACCCWGTGACATGGTATTAGTCAAGTCCCTTCCTTAAT 5340
Qy |||||
Db 5341 CCCCATCCCTAGATACATCTCGGGAAGGACCCCTACCCAGTCATTTTATYACCCCAACTG 5400
Qy |||||
Db 5341 CCCCATCCCTAGATACATCTCGGGAAGGACCCCTACCCAGTCATTTTATYACCCCAACTG 5400
Qy |||||
Db 5401 CGGTTAAAGTGGCTGGAGTGAGTCTTGGATACATCACTTGGTCAAAATCTCTGGATAC 5460
Qy |||||

Db 5401 CGGTTAAAGTGGCTGGAGTGGAGTCTTGGATACATCACACTTGAGTCAAAATCTCGATAC 5460
Qy |||||
Db 5461 TGCCAAAGGAAACCTGAAAAATCCAGAGAGACAAACCTAGCTATTCTCTGGAACCTCTAGAGG 5520
Qy |||||
Db 5461 TGCCAAAGGAAACCTGAAAAATCCAGAGAGACAAACCTAGCTATTCTCTGGAACCTCTAGAGG 5520
Qy |||||
Db 5521 ATTTGGCGCTGCTCTTTCAAAACAAACACAGGAGGAAAGTAATCTAAATCATAAATCCCC 5580
Qy |||||
Db 5521 ATTTGGCGCTGCTCTTTCAAAACAAACACAGGAGGAAAGTAATCTAAATCATAAATCCCC 5580
Qy |||||
Db 5581 ATGGSCTCCCTTATCATATTTTCTCTKTASTGTSTTTTACCTSTTTTCACTCTCACT 5640
Qy |||||
Db 5581 ATGGSCTCCCTTATCATATTTTCTCTKTASTGTSTTTTACCTSTTTTCACTCTCACT 5640
Qy |||||
Db 5641 GCACCCCTCCATGCGCGCTGTATGACAGTAGTCTCCCTTACCMAGAGTTTCTATGGAGA 5700
Qy |||||
Db 5641 GCACCCCTCCATGCGCGCTGTATGACAGTAGTCTCCCTTACCMAGAGTTTCTATGGAGA 5700
Qy |||||
Db 5701 ATGACGCGTCCCGGAAATATTTGATGCCCATGTATAGAGTCTTTTAAAGGAAACCCCC 5760
Qy |||||
Db 5701 ATGACGCGTCCCGGAAATATTTGATGCCCATGTATAGAGTCTTTTAAAGGAAACCCCC 5760
Qy |||||
Db 5761 ACCTTCACTGCCACACCCCATATGCGCGCTGCTATCAGTCTGCACTCTTTGCATG 5820
Qy |||||
Db 5761 ACCTTCACTGCCACACCCCATATGCGCGCTGCTATCAGTCTGCACTCTTTGCATG 5820
Qy |||||
Db 5821 CATGCAAAATACATCATTTATTTGGACAGGAAAAATGATTAATCTAGTTTCTCTGAGGACTT 5880
Qy |||||
Db 5821 CATGCAAAATACATCATTTATTTGGACAGGAAAAATGATTAATCTAGTTTCTCTGAGGACTT 5880
Qy |||||
Db 5881 GGAGTCACTGTCTGTGGACTTACTTTTCAACCCAACTGGTATGTCTGATGGGGTGGAGTT 5940
Qy |||||
Db 5881 GGAGTCACTGTCTGTGGACTTACTTTTCAACCCAACTGGTATGTCTGATGGGGTGGAGTT 5940
Qy |||||
Db 5941 CAGATCAGGCAAGAGAAAAATGTAAGAAGTAATCTCCCAACTCAACCCSGGTACAT 6000
Qy |||||
Db 5941 CAGATCAGGCAAGAGAAAAATGTAAGAAGTAATCTCCCAACTCAACCCSGGTACAT 6000
Qy |||||
Db 6001 GGCACTCTAGCCCTTACAAAGGACTAGATCTCTCAAACTACATGAAACCTCTCGTACC 6060
Qy |||||
Db 6001 GGCACTCTAGCCCTTACAAAGGACTAGATCTCTCAAACTACATGAAACCTCTCGTACC 6060
Qy |||||
Db 6061 CATACTCGCTGTGTAAGCTTATTAATACCACTCTCACTGGGCTCCTAGAGTCTCGGCC 6120
Qy |||||
Db 6061 CATACTCGCTGTGTAAGCTTATTAATACCACTCTCACTGGGCTCCTAGAGTCTCGGCC 6120
Qy |||||
Db 6121 CAAAACCTTACTAACTTGTGGATATGCTCCCTGAACTTTCARGCCATATGTTTCAATC 6180
Qy |||||
Db 6121 CAAAACCTTACTAACTTGTGGATATGCTCCCTGAACTTTCARGCCATATGTTTCAATC 6180
Qy |||||
Db 6181 CCTGTACTGAAACAAATGGAAACAACTTTCAGCAAGAAATAAACACCACTTCCGTTTTAGTA 6240
Qy |||||
Db 6181 CCTGTACTGAAACAAATGGAAACAACTTTCAGCAAGAAATAAACACCACTTCCGTTTTAGTA 6240
Qy |||||
Db 6241 GGAACCTCTGTTTCCAAATSTGAAAAAACCATACTCAAAACCTCACTGTGTAAATTTT 6300
Qy |||||
Db 6241 GGAACCTCTGTTTCCAAATSTGAAAAAACCATACTCAAAACCTCACTGTGTAAATTTT 6300
Qy |||||
Db 6301 AGCAATCTACTACATACAAACCAACTCCCAATGATCAGGTGGGTAACTCCCTCCACACAA 6360
Qy |||||
Db 6301 AGCAATCTACTACATACAAACCAACTCCCAATGATCAGGTGGGTAACTCCCTCCACACAA 6360
Qy |||||
Db 6361 ATAGTCTGCGCTACCTCAGGAATATTTTGTCTGTGTAGTACCTCAGGCTATCGTTGTTG 6420
Qy |||||
Db 6361 ATAGTCTGCGCTACCTCAGGAATATTTTGTCTGTGTAGTACCTCAGGCTATCGTTGTTG 6420
Qy |||||
Db 6421 AATGGCTCTTCAAGATCTATGTGCTTCTCTCAATCTTAGTGCCCCCYATGRCATCTAC 6480
Qy |||||
Db 6421 AATGGCTCTTCAAGATCTATGTGCTTCTCTCAATCTTAGTGCCCCCYATGRCATCTAC 6480
Qy |||||
Db 6481 ACTGAAACAGATTTTATACAGTTATGTCATATCTAAGCCCCGCAACAAAGATACCCATT 6540
Qy |||||
Db 6481 ACTGAAACAGATTTTATACAGTTATGTCATATCTAAGCCCCGCAACAAAGATACCCATT 6540
Qy |||||

Db	2581	AAGCCCAAGGCTTAGTAAACCAATGATTAACCTCCCTGCAAGTAATTCGCTAGTGGATTGAG	2640
Qy	2641	GAGGCACAGAAACCCAGTGGGACAGTGGAGGGTTAGTGCAGAGATCTCAGGATTTATCAATGG	2700
Db	2641	GAGGCACAGAAACCCAGTGGGACAGTGGAGGGTTAGTGCAGAGATCTCAGGATTTATCAATGG	2700
Qy	2701	AGGCGGTTGCTCTTTATACCCAGCTGTACCTAGCCCTTATACCTGTGMYTTCCCAATAC	2760
Db	2701	AGGCGGTTGCTCTTTATACCCAGCTGTACCTAGCCCTTATACCTGTGMYTTCCCAATAC	2760
Qy	2761	CAGAGGACAGAGGTTTACSTCCCTGGACCTTMAGGATGCTCTTCTGCAATCCCTG	2820
Db	2761	CAGAGGACAGAGGTTTACSTCCCTGGACCTTMAGGATGCTCTTCTGCAATCCCTG	2820
Qy	2821	TACATCCTGACTCTCAATCTCTGTTGCTTTGAAAGTACTTCAAAACCCATCTCAAC	2880
Db	2821	TACATCCTGACTCTCAATCTCTGTTGCTTTGAAAGTACTTCAAAACCCATCTCTCAAC	2880
Qy	2881	TCACCTGGACTCTTTTACCCCAAGGTTTACGGGATAGTCCCATCTATTTGGCCAGGCAT	2940
Db	2881	TCACCTGGACTCTTTTACCCCAAGGTTTACGGGATAGTCCCATCTATTTGGCCAGGCAT	2940
Qy	2941	TAGCCCAAGACTTGAGYCARITYMTACCTGGACACTCTTGTCTCTCRGTAKGTGGATG	3000
Db	2941	TAGCCCAAGACTTGAGYCARITYMTACCTGGACACTCTTGTCTCTCRGTAKGTGGATG	3000
Qy	3001	ATTTACTTTTGGCTTTCAGAAACCTTGTGCAATCAAGCCACCAAGCRCTCTTMA	3060
Db	3001	ATTTACTTTTGGCTTTCAGAAACCTTGTGCAATCAAGCCACCAAGCRCTCTTMA	3060
Qy	3061	ATTTCCTCGYACCTGTGGCTTACAWGGTTTCCAAACCSARAGCTCARCTCTGTCTCACAGC	3120
Db	3061	ATTTCCTCGYACCTGTGGCTTACAWGGTTTCCAAACCSARAGCTCARCTCTGTCTCACAGC	3120
Qy	3121	AGSTTAAATACTTAGGCTAARATTTATCCAAAGGCACTAAGGRCRTCTTGA	3180
Db	3121	AGSTTAAATACTTAGGCTAARATTTATCCAAAGGCACTAAGGRCRTCTTGA	3180
Qy	3181	TCAGGCTTACTTGGCTTATCTCATCYCAAAACCTTAAAGGCACTAAGGRCRTCTTGA	3240
Db	3181	TCAGGCTTACTTGGCTTATCTCATCYCAAAACCTTAAAGGCACTAAGGRCRTCTTGA	3240
Qy	3241	GCRTAAYAGGYTTCTGCGGAATGATTTCCAGAGTGTGGCRAAATAGCCAGGYCATTA	3300
Db	3241	GCRTAAYAGGYTTCTGCGGAATGATTTCCAGAGTGTGGCRAAATAGCCAGGYCATTA	3300
Qy	3301	WATACASTAATTAAGGAACTCAGAAAGCAATACCCATTTARTTAAGATGGAYAMCTGAA	3360
Db	3301	WATACASTAATTAAGGAACTCAGAAAGCAATACCCATTTARTTAAGATGGAYAMCTGAA	3360
Qy	3361	GYMRAAGTGGCTTTCCAGGCCCCCTTAAAGAGGCTTAAACCCAGYCCCAGTGTAAGYT	3420
Db	3361	GYMRAAGTGGCTTTCCAGGCCCCCTTAAAGAGGCTTAAACCCAGYCCCAGTGTAAGYT	3420
Qy	3421	TGCAACRGGGCAAGACTTTTSTTYATVARTCAGAGAAACCAAGAAVAGCTCTRGGG	3480
Db	3421	TGCAACRGGGCAAGACTTTTSTTYATVARTCAGAGAAACCAAGAAVAGCTCTRGGG	3480
Qy	3481	GTCTTTACAGRTCCRAGGAYGAGCTTGCACACCTTGTGCRVACCTGASTAGGAAAYT	3540
Db	3481	GTCTTTACAGRTCCRAGGAYGAGCTTGCACACCTTGTGCRVACCTGASTAGGAAAYT	3540
Qy	3541	GATGTAGTGGCAAGGTTGRCYTCATCTGTTAYGGGTAGTGTGCGAGTAGCAGTYKTA	3600
Db	3541	GATGTAGTGGCAAGGTTGRCYTCATCTGTTAYGGGTAGTGTGCGAGTAGCAGTYKTA	3600
Qy	3601	GTATCTGAAGCAGTAAATATAACAGGGRAGAGATCTTACTGTGTGGACATCTCATGAK	3660
Db	3601	GTATCTGAAGCAGTAAATATAACAGGGRAGAGATCTTACTGTGTGGACATCTCATGAK	3660
Qy	3661	GTGAAYRGCACTACTGCTAAAGGAGACTTGTGGCTGTGAGCACTGTTTACTTAA	3720
Db	3661	GTGAAYRGCACTACTGCTAAAGGAGACTTGTGGCTGTGAGCACTGTTTACTTAA	3720
Qy	3721	TRTCAGGCTCTATTTACTTGAAGGCGAGTGTGTCRACCTGTGCACTGTGCAACTCTTAAAC	3780
Db	3721	TRTCAGGCTCTATTTACTTGAAGGCGAGTGTGTCRACCTGTGCACTGTGCAACTCTTAAAC	3780
Qy	3781	CCAGYCNCACTTCTTCAGAGCAATGAAGAAAGATARAAYATACTGTCAACAARTATTT	3840
Db	3781	CCAGYCNCACTTCTTCAGAGCAATGAAGAAAGATARAAYATACTGTCAACAARTATTT	3840
Qy	3841	TCTCAAAACCTATGCACTCGAGGGAACCTTCTTAGAGTTCCTTGTGACTGATCCYGCACCTT	3900
Db	3841	TCTCAAAACCTATGCACTCGAGGGAACCTTCTTAGAGTTCCTTGTGACTGATCCYGCACCTT	3900
Qy	3901	CAACTTGTATATGATGGAAGTTCCTTTGTAGAAAAGGACTTCGAAAAGYGGGTATGC	3960
Db	3901	CAACTTGTATATGATGGAAGTTCCTTTGTAGAAAAGGACTTCGAAAAGYGGGTATGC	3960
Qy	3961	AGTGGTCAGTGATTAATGGAATATTTGAAAGTAACTCCCTCCTCAGTCCAGGAACTAGTCTYA	4020
Db	3961	AGTGGTCAGTGATTAATGGAATATTTGAAAGTAACTCCCTCCTCAGTCCAGGAACTAGTCTYA	4020
Qy	4021	GCTRGCAAGAACTAATAGCCCTCACTGAGGCACTAGAAATTAAGGAAAGAAAAGGGYAAA	4080
Db	4021	GCTRGCAAGAACTAATAGCCCTCACTGAGGCACTAGAAATTAAGGAAAGAAAAGGGYAAA	4080
Qy	4081	TATATATACAGACTCTTRATATGCTTACCTAGTCTCCTCCTCAGTCCAGGAACTAGTCTYA	4140
Db	4081	TATATATACAGACTCTTRATATGCTTACCTAGTCTCCTCCTCAGTCCAGGAACTAGTCTYA	4140
Qy	4141	AGAAAGGAACTTCTTAACTTCYAGGAAACACTATCMACATCAGGAAAGCCATTAGGAR	4200
Db	4141	AGAAAGGAACTTCTTAACTTCYAGGAAACACTATCMACATCAGGAAAGCCATTAGGAR	4200
Qy	4201	ATTATATTGCGGTACAGAAACCTTARAGAGGTGGMAGTCTTACACTGCTGCGGTCTATCA	4260
Db	4201	ATTATATTGCGGTACAGAAACCTTARAGAGGTGGMAGTCTTACACTGCTGCGGTCTATCA	4260
Qy	4261	NAAGGAAAGAAAGGAAATASAGGAAATGCGCAAGCAKATATTTGAAGCAAAAGAGC	4320
Db	4261	NAAGGAAAGAAAGGAAATASAGGAAATGCGCAAGCAKATATTTGAAGCAAAAGAGC	4320
Qy	4321	TGCAAGGAGGAGCCCTTCAATAGAAATGCTTATTAACCTTCCCTTATAGTATAGGTAATCC	4380
Db	4321	TGCAAGGAGGAGCCCTTCAATAGAAATGCTTATTAACCTTCCCTTATAGTATAGGTAATCC	4380
Qy	4381	CTTCCGGGAAACCAAGCCCCAGTACTCAGCAGGAGAAACAGAAATGGGAAACCTCACAGG	4440
Db	4381	CTTCCGGGAAACCAAGCCCCAGTACTCAGCAGGAGAAACAGAAATGGGAAACCTCACAGG	4440
Qy	4441	CAGTTTTCTCCCTCGGAGCGGTAGCCACTGAGAGGAGAAATATCTTTTGCCTGCAAC	4500
Db	4441	CAGTTTTCTCCCTCGGAGCGGTAGCCACTGAGAGGAGAAATATCTTTTGCCTGCAAC	4500
Qy	4501	TATCAATGGAATTTACTTAAACCTTCAATCAACCTTTCCTTATAGGATCGATAGCAC	4560
Db	4501	TATCAATGGAATTTACTTAAACCTTCAATCAACCTTTCCTTATAGGATCGATAGCAC	4560
Qy	4561	CCATCARATGGCAATCAATTTTACTGGAACAGGCTTTTCAAACTTATCAAGCARAT	4620
Db	4561	CCATCARATGGCAATCAATTTTACTGGAACAGGCTTTTCAAACTTATCAAGCARAT	4620
Qy	4621	AKTCAAGGCTGTGAATGTGCAARAAATATCCCTGCTCTATCGCAAGCTCTTTC	4680
Db	4621	AKTCAAGGCTGTGAATGTGCAARAAATATCCCTGCTCTATCGCAAGCTCTTTC	4680
Qy	4681	AGGAAACAAAPAAACAGGCAATTCCTGCAACCTGGAACCTGATTTTACCAACAG	4740
Db	4681	AGGAAACAAAPAAACAGGCAATTCCTGCAACCTGGAACCTGATTTTACCAACAG	4740
Qy	4741	CCCAACCTCAGGGATTTTCACTATCTACTAGTCTGGGTARATATCTTTCACGGGTGGGCA	4800
Db	4741	CCCAACCTCAGGGATTTTCACTATCTACTAGTCTGGGTARATATCTTTCACGGGTGGGCA	4800

Qy	4801	RAGSCCTTCCCTGTAGGACAGAAAAGCCCAAGAGGTAAATAAAGGCACCTAGTTTCATGAA	4860	Db	5881	GGAGTCACTGTCTGTGGACTTACTTCCACCAACTGGTATGTCTGATGGGGTGGAGTT	5940
Db	4801	RAGSCCTTCCCTGTAGGACAGAAAAGCCCAAGAGGTAAATAAAGGCACCTAGTTTCATGAA	4860	Qy	5941	CAAGATCAGGCAAGAGAAAACATGTAAAAGAGTAACTCCCAACTCCACCGGGTACAT	6000
Qy	4861	ATAATTCACAGATTCGGACTTCCCGAGGCTTACAGAGTGACATAGCCCTGCTTCCAG	4920	Db	5941	CAAGATCAGGCAAGAGAAAACATGTAAAAGAGTAACTCCCAACTCCACCGGGTACAT	6000
Db	4861	ATAATTCACAGATTCGGACTTCCCGAGGCTTACAGAGTGACATAGCCCTGCTTCCAG	4920	Qy	6001	GGCACCTCTAGCCCTCAAAAGGACTAGATCTCTCAAAACTACATGAAAACCTCCGTAAC	6060
Qy	4921	GCACAGTAAACCCAGGAGATATCCAGCGTTAGGTATACGATATCACTTACATCGGCC	4980	Db	6001	GGCACCTCTAGCCCTCAAAAGGACTAGATCTCTCAAAACTACATGAAAACCTCCGTAAC	6060
Db	4921	GCACAGTAAACCCAGGAGATATCCAGCGTTAGGTATACGATATCACTTACATCGGCC	4980	Qy	6061	CATACTCGCTGTGTAAGCCTATTATTAACACCCCTCACTGGGCTCCATGAGGTCTCGGCC	6120
Qy	4981	TGAAGGCCACAGTCCTCAGGGAAGGTGAGAAAATGAATGAAAACVCTCAAAGGACATCTA	5040	Db	6061	CATACTCGCTGTGTAAGCCTATTATTAACACCCCTCACTGGGCTCCATGAGGTCTCGGCC	6120
Db	4981	TGAAGGCCACAGTCCTCAGGGAAGGTGAGAAAATGAATGAAAACVCTCAAAGGACATCTA	5040	Qy	6121	CAAAACCTACTAACTGTGTGATATGCTCCCTGAACTTCARGCCATATGTTTCAATC	6180
Qy	5041	AAAAAGCAAAACCCAGGAAACCCACCTCACATGGCCTGTCTGTGCTATAGCCCTTAAA	5100	Db	6121	CAAAACCTACTAACTGTGTGATATGCTCCCTGAACTTCARGCCATATGTTTCAATC	6180
Db	5041	AAAAAGCAAAACCCAGGAAACCCACCTCACATGGCCTGTCTGTGCTATAGCCCTTAAA	5100	Qy	6181	CCTGTACTCTGAACAATGGAAACAACTTCAGCAACAGAAAATAAACCACTTCGGTTTTAGTA	6240
Qy	5101	AGAACTGCAACTTTCACCAAAAGCAGGACTTAGCCCATACGAAATGCTGTATGGGAAG	5160	Db	6181	CCTGTACTCTGAACAATGGAAACAACTTCAGCAACAGAAAATAAACCACTTCGGTTTTAGTA	6240
Db	5101	AGAACTGCAACTTTCACCAAAAGCAGGACTTAGCCCATACGAAATGCTGTATGGGAAG	5160	Qy	6241	GGACCTCTGTTTCCAAATSTGGAAATACCCATACCTCAAACTCACTGTGTAATAATTT	6300
Qy	5161	CCCTTCATAACCAATGACCTTGTGCTTGACCAAGACAGCCAACTTAGTTGCGACATCA	5220	Db	6241	GGACCTCTGTTTCCAAATSTGGAAATACCCATACCTCAAACTCACTGTGTAATAATTT	6300
Db	5161	CCCTTCATAACCAATGACCTTGTGCTTGACCAAGACAGCCAACTTAGTTGCGACATCA	5220	Qy	6301	AGCAATACTACATACACAACTCCCAATGATCAGGTGGGTAACTCTCTCCACACAA	6360
Qy	5221	CCTCCTTAGCCAAATATCAAGTCTTAAAACATTTACAGGAACCTATCCCTGAGAG	5280	Db	6301	AGCAATACTACATACACAACTCCCAATGATCAGGTGGGTAACTCTCTCCACACAA	6360
Db	5221	CCTCCTTAGCCAAATATCAAGTCTTAAAACATTTACAGGAACCTATCCCTGAGAG	5280	Qy	6361	ATAGTCTGCCTACCCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATPCGTTGTTG	6420
Qy	5281	AGGAAAAGAACTATTCACCCWGTGACATGTTAGTCAAGTCCCTTCYCTCTAATT	5340	Db	6361	ATAGTCTGCCTACCCCTCAGGAATATTTTTGTCTGTGGTACCTCAGCCTATPCGTTGTTG	6420
Db	5281	AGGAAAAGAACTATTCACCCWGTGACATGTTAGTCAAGTCCCTTCYCTCTAATT	5340	Qy	6421	AATGGCTCTCAGAACTATGCTGCTCCTCTCATTTCTTAGTGCCCCVATGRCCTATAC	6480
Qy	5341	CCCATCCCTAGATACATCTCTGGGAAGACCCCTACCCAGTCATTTTTATYTTACCCAACTG	5400	Db	6421	AATGGCTCTCAGAACTATGCTGCTCCTCTCATTTCTTAGTGCCCCVATGRCCTATAC	6480
Db	5341	CCCATCCCTAGATACATCTCTGGGAAGACCCCTACCCAGTCATTTTTATYTTACCCAACTG	5400	Qy	6481	ACTGMAACAGATTTATACAGTTATGTCATATCTAAGCCCGCAACAAAAGAGTACCCATT	6540
Qy	5401	CGGTAAAGTGGCTGGAGTGAGCTTGGATACATCACATTTGATCAAACTCTGGATAC	5460	Db	6481	ACTGMAACAGATTTATACAGTTATGTCATATCTAAGCCCGCAACAAAAGAGTACCCATT	6540
Db	5401	CGGTAAAGTGGCTGGAGTGAGCTTGGATACATCACATTTGATCAAACTCTGGATAC	5460	Qy	6541	CTTCTTTTGTATPAGAGCAGGAGTCTAGGTGCACTAGGTACTGGAATGCGGGGTATC	6600
Qy	5461	TGCCAAAGAACTCTGAAAATCCAGAGAACAGCTAGCTATTTCTGTGAACTCTAGAGG	5520	Db	6541	CTTCTTTTGTATPAGAGCAGGAGTCTAGGTGCACTAGGTACTGGAATGCGGGGTATC	6600
Db	5461	TGCCAAAGAACTCTGAAAATCCAGAGAACAGCTAGCTATTTCTGTGAACTCTAGAGG	5520	Qy	6601	ACAACTCTACTCAGTTCTACTACAACTATCTCAAGAACTTAAATGGGACATGGAACGG	6660
Qy	5521	ATTTGCGCTGCTCTTCAAAACAAACACAGGAGGAAAGTAACTAAAATCATAAATCCCCC	5580	Db	6601	ACAACTCTACTCAGTTCTACTACAACTATCTCAAGAACTTAAATGGGACATGGAACGG	6660
Db	5521	ATTTGCGCTGCTCTTCAAAACAAACACAGGAGGAAAGTAACTAAAATCATAAATCCCCC	5580	Qy	6661	GTCCCGACTCCCTGGTCACTTCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCTCTT	6720
Qy	5581	ATGSGCTCCCTTATCATATTTTCTCTKTASTGTTSTTTTACCTSTTTTCACTCTCACT	5640	Db	6661	GTCCCGACTCCCTGGTCACTTCAAGATCAACTTAACTCCCTAGCAGCAGTAGTCTCTT	6720
Db	5581	ATGSGCTCCCTTATCATATTTTCTCTKTASTGTTSTTTTACCTSTTTTCACTCTCACT	5640	Qy	6721	CRAAATCGAAGAGCTTTAGCTYCTAAACCGCTCAAGAGGGGAAACCTGTTTATTTTTA	6780
Qy	5641	GCACCCCCTCATGCGCTGTATGACACAGTACCTCCCTYACCMAGAGTTCTATGGAGA	5700	Db	6721	CRAAATCGAAGAGCTTTAGCTYCTAAACCGCTCAAGAGGGGAAACCTGTTTATTTTTA	6780
Db	5641	GCACCCCCTCATGCGCTGTATGACACAGTACCTCCCTYACCMAGAGTTCTATGGAGA	5700	Qy	6781	GGGGAAGAATGCTGTTTATTTATGTTAACTCCCGAATCGTCACTGAGAAAGTTPAAGAA	6840
Qy	5701	ATGACAGCTCCCGGAAATATTTGATGCCCCATCGTATAGGAGTCTTTTAAAGGGAACCCCC	5760	Db	6781	GGGGAAGAATGCTGTTTATTTATGTTAACTCCCGAATCGTCACTGAGAAAGTTPAAGAA	6840
Db	5701	ATGACAGCTCCCGGAAATATTTGATGCCCCATCGTATAGGAGTCTTTTAAAGGGAACCCCC	5760	Qy	6841	ATTCSAGATCGAATACAACTAGACAGAGAGCTTCGAAACACTGGACCTCGGGGCTC	6900
Qy	5761	ACCTTCACTGCCCAACACCATATGCCCCGCAACTGCTATCACTCTGCCCACTCTTTGCATG	5820	Db	6841	ATTCSAGATCGAATACAACTAGACAGAGAGCTTCGAAACACTGGACCTCGGGGCTC	6900
Db	5761	ACCTTCACTGCCCAACACCATATGCCCCGCAACTGCTATCACTCTGCCCACTCTTTGCATG	5820	Qy	6901	CTCAGCCRAATGGATGCGCTTGAATTCCTCCCTTCTTAGGACCTCTAGCAGCTATATATTTG	6960
Qy	5821	CATGCAATACTCATTTATGGACAGGAAAATGATTAATCTTAGTTGCTCTGGAGACTT	5880	Db	6901	CTCAGCCRAATGGATGCGCTTGAATTCCTCCCTTCTTAGGACCTCTAGCAGCTATATATTTG	6960
Db	5821	CATGCAATACTCATTTATGGACAGGAAAATGATTAATCTTAGTTGCTCTGGAGACTT	5880	Qy	6961	CTACTCTCTTTGGACCTCTGTTTACCTCTGTTTAACTTTGTTCTCTTCCAGAAATC	7020
Qy	5881	GGAGTCACTGTCTGTGGACTTACTTCCACCAACTGGTATGTTCTGATGGGGTGGAGTT	5940				

6961 CTACTCTCTTTGGACCTGTATCTTTTACCTCTCTTGTAACTTTGTCTCTTCAGAAATC 7020
 7021 GAAGCTGTTAACTTACAAATGGAGCCCAAGATGAGTCCAGACTTAAGATCTACCGCAGA 7080
 7021 GAAGCTGTTAACTTACAAATGGAGCCCAAGATGAGTCCAGACTTAAGATCTACCGCAGA 7080
 7081 CCCTTGACCGGGCTGTAGCCACAGATCTGATTTAATGACATCAAAAGGACCCCTCTCT 7140
 7081 CCCTTGACCGGGCTGTAGCCACAGATCTGATTTAATGACATCAAAAGGACCCCTCTCT 7140
 7141 GAGGAATCTCAGCTGCACAACTCTACTAGCCCAATTCAGCAGGAAGCAGTTAGAGC 7200
 7141 GAGGAATCTCAGCTGCACAACTCTACTAGCCCAATTCAGCAGGAAGCAGTTAGAGC 7200
 7201 GGTSGTCGGCAACCTCCCAACAGACTTGTAGTTTCTGTTGAGATGGGGACCTGAGA 7260
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 7261 GACAGGACTAGCTGGATTTCTTAGGCTGATTAAGAAATCCYTAAGCCTTAGSTGGGAAGGTG 7320
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RESULT 3
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 ACCESSION AX000966
 VERSION AX000966.1 GI:7241208
 KEYWORDS
 SOURCE unidentified
 ORGANISM unidentified
 unclassified.
 REFERENCE 1 (bases 1 to 7582)
 AUTHORS Beseme, F. and Blond, J.
 TITLE ENDOGENETIC RETROVIRAL SEQUENCES, ASSOCIATED WITH AUTOIMMUNE DISEASES OR WITH PREGNANCY DISORDERS
 JOURNAL Patent: WO 9902696-A 11 21-JAN-1999;
 BIO MERIEUX (FR); BESEME FREDERIC (FR)
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QY	1321	GAAGGAAGANAATGATTTCCCCACAGCCAGCARGCAGTTTCCCGTCTASACCTCATTTG	1380	Db	2401	CTGTCTTGAGGAAGAAATTAATCTCTGAACTCTGGGCAACAGAAAGCAATATGAGACGAGC	2460
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QY	1501	ACACAGGGGAAGGAAGAAATCTACTGCTTTCTGGAGAGACTAAGGGAGCATTTGAG	1560	Db	2581	AAGCCCAAGGCTTAGTAAACCAATGCAATCTCCCTGCAAGTAATTCGGTAGTGATGAG	2640
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QY	1561	GAAGCGTCCCTCTCTGTGACCTGATCTTCTGAAGGCCAACTAATCTTAAAGCGTAAGTT	1620	Db	2641	GAGGCACAGAAACCCAGTGGACAGTGGAGGTTAGTGCAGATCTCAGGATTAATCAATGG	2700
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QY	1621	TATCACTCACTCAGCTCAGACATTAAGAAAACTTCAAAAGCTGCGGTAGGCCCGGAG	1680	Db	2701	AGGCCGTTGCTTTTATATACCCAGCTGTACTAGCCCTTATCTACTGTGMYTTCCCAATAC	2760
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QY	2041	AGGTTGCTTGGGCAAGCGCCATCCCATGCCATCAACCTTCAAGAGCCCTGGGTATGCTT	2100	Db	3121	AGGTTAAATCTTAGGCTAARATTTATCCAAAGGCACARGGCCCTCAGTGAGGAARYA	3180
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RESULT 4

AX027480

LOCUS

DEFINITION

ACCESSION

Sequence 30 from Patent FR2788784.

AX027480

7582 bp

DNA

linear

PAT 16-SEP-2000

VERSION	AX027480.1	GI:10188444
KEYWORDS	Homo sapiens (human)	
SOURCE	Homo sapiens	
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
REFERENCE	1 Mallet, F., Voisset, C. and Paranhos, B. G.	
AUTHORS	Patent: FR 2788784-A 30 28-JUL-2000;	
JOURNAL	BIO MERIEUX (FR)	
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QY	421	TGGCCCAAGATTCCATTCTTGGATCCGTGAGGSCAAGAACTCCAGGTCAGAGATAC 480
DB	421	TGGCCCAAGATTCCATTCTTGGATCCGTGAGGSCAAGAACTCCAGGTCAGAGATAC 480
QY	481	GARGCTTGCCACCATCTTGGAAAGCGGCTGTACCTCTTGGAAAGTGGTTCAACCACTC 540
DB	481	GARGCTTGCCACCATCTTGGAAAGCGGCTGTACCTCTTGGAAAGTGGTTCAACCACTC 540
QY	541	TTGGAGCTCTGTGAGCAAGGACCCCGGTTACATTCTTGGGACCCMSRACGGACATCC 600
DB	541	TTGGAGCTCTGTGAGCAAGGACCCCGGTTACATTCTTGGGACCCMSRACGGACATCC 600
QY	601	MAAGTGATGGGAAACCTTCCCGCAAGACAAACCGCCCTAAGACGTTATCTCGGARAAT 660
DB	601	MAAGTGATGGGAAACCTTCCCGCAAGACAAACCGCCCTAAGACGTTATCTCGGARAAT 660
QY	661	TGGGACAAATTTGACCTCAGACCTAAGAAAGAAACGACTTATATCTCTGCAAGTCC 720
DB	661	TGGGACAAATTTGACCTCAGACCTAAGAAAGAAACGACTTATATCTCTGCAAGTCC 720
QY	721	GCCTGGCACTCTGAGGAGTATAAATTAACCATCTTACAGCTAGACCTTTCTTTG 780
DB	721	GCCTGGCACTCTGAGGAGTATAAATTAACCATCTTACAGCTAGACCTTTCTTTG 780
QY	781	TAGAAAGGCAATGGAGTGAAGTGCATTAAGTACAAACTTTCTTTTCAATTAAGAGCAA 840
DB	781	TAGAAAGGCAATGGAGTGAAGTGCATTAAGTACAAACTTTCTTTTCAATTAAGAGCAA 840
QY	841	CTCACAATATTGTAAAAAGTGTGATTTATCCCTTACAGGAGGCTTCCAGAGTCTACCTCC 900
DB	841	CTCACAATATTGTAAAAAGTGTGATTTATCCCTTACAGGAGGCTTCCAGAGTCTACCTCC 900
QY	901	CTATCCAGCATCCCGGACTCTTCCCAATTAAGGACCCCTTCAACCCCAATGG 960
DB	901	CTATCCAGCATCCCGGACTCTTCCCAATTAAGGACCCCTTCAACCCCAATGG 960
QY	961	TCCAAAGGAGTAGACAAAGGGTAAACAGTGAAACAAAGAGTGCCCAATATTTCCCAAT 1020
DB	961	TCCAAAGGAGTAGACAAAGGGTAAACAGTGAAACAAAGAGTGCCCAATATTTCCCAAT 1020
QY	1021	TATGACCCCTTCCCAAGCAGTGGGAGGAAGAAATTCGGCCAGCCAGAGTGCAATGTCYT 1080
DB	1021	TATGACCCCTTCCCAAGCAGTGGGAGGAAGAAATTCGGCCAGCCAGAGTGCAATGTCYT 1080
QY	1081	TTTTYTCCTCCAGACTTAAAGCAAAATAAACAAGACTTAGGTAAATTTCTCAGATAATYCT 1140
DB	1081	TTTTYTCCTCCAGACTTAAAGCAAAATAAACAAGACTTAGGTAAATTTCTCAGATAATYCT 1140
QY	1141	GATGGCTATATTGRTGTTTTTAAGGGTTAGGCAAAATTTCTTGATCTGACATGGAGAT 1200
DB	1141	GATGGCTATATTGRTGTTTTTAAGGGTTAGGCAAAATTTCTTGATCTGACATGGAGAT 1200
QY	1201	ATATATGTCACCTGCTAAATCAGACACTAACCCCAATAGAGAAGTGCCACCACTAATGTC 1260
DB	1201	ATATATGTCACCTGCTAAATCAGACACTAACCCCAATAGAGAAGTGCCACCACTAATGTC 1260
QY	1261	AGCTGAGGTTTGGGATCTCTGATCTCAGTCAAGTCAATGGATANGGATGACAACA 1320
DB	1261	AGCTGAGGTTTGGGATCTCTGATCTCAGTCAAGTCAATGGATANGGATGACAACA 1320
QY	1321	GAAGGAAAGANAATGATTTCCCAAGGCGAGCAGTGATCCAGTCTASACCTCATTTG 1380
DB	1321	GAAGGAAAGANAATGATTTCCCAAGGCGAGCAGTGATCCAGTCTASACCTCATTTG 1380
QY	1381	GGGACACAGAAATCAGTAACATGGGAGATTGGTGCTGCAGACATTTGCTAACTTGTGTC 1440
DB	1381	GGGACACAGAAATCAGTAACATGGGAGATTGGTGCTGCAGACATTTGCTAACTTGTGTC 1440
QY	1441	TASAAAGACTAAGGAAAATCTAGSAAAGAAATCTAAGAAATTTCAATGATGTCCACATA 1500
DB	1441	TASAAAGACTAAGGAAAATCTAGSAAAGAAATCTAAGAAATTTCAATGATGTCCACATA 1500
QY	1501	ACACAGGGGAGGGAAGAAATCTTACCTGCTTTCTGGAGAGACTAAGGGAGGCAATGAG 1560
DB	1501	ACACAGGGGAGGGAAGAAATCTTACCTGCTTTCTGGAGAGACTAAGGGAGGCAATGAG 1560
QY	1561	GAAGGCTGCTCTCTGTGCTACCTGCTCTTCTGAAGGCCAATTAATCTTAAAGCGTAAATT 1620
DB	1561	GAAGGCTGCTCTCTGTGCTACCTGCTCTTCTGAAGGCCAATTAATCTTAAAGCGTAAATT 1620
QY	1621	TATCACTCAGTCACTGAGCACTTAAAGAAAATCTTCAAAAGTCTGCGGTAGGCGCGAG 1680
DB	1621	TATCACTCAGTCACTGAGCACTTAAAGAAAATCTTCAAAAGTCTGCGGTAGGCGCGAG 1680
QY	1681	CABAACCTTAGAACCCTATTGAATCTTGGCAACTTCGGTTTTTTTATTAATAGAGATCAGGAG 1740
DB	1681	CABAACCTTAGAACCCTATTGAATCTTGGCAACTTCGGTTTTTTTATTAATAGAGATCAGGAG 1740
QY	1741	GAGCAGGCGGAACAGGACAAACCGGATTAAGAAAAGGCCACCGCTTTAGTCATGCCCT 1800
DB	1741	GAGCAGGCGGAACAGGACAAACCGGATTAAGAAAAGGCCACCGCTTTAGTCATGCCCT 1800
QY	1801	CAGGCAAGTGAATTTGGAGGCTCTGGAAGGGAAGAGCTGGGCAAAATTAATGCTCTAA 1860
DB	1801	CAGGCAAGTGAATTTGGAGGCTCTGGAAGGGAAGAGCTGGGCAAAATTAATGCTCTAA 1860
QY	1861	TAGGGCTGCTTCCAGTGGGCTCTACAGGACACTTTTAAAAAGATTTGCTCCAGTAGAAG 1920

QY	4081	TATATATACAGACTCTTARTATGCTYACCTAGTCTNTCCATGCCCATGMRGCAATATGSAR	4140
Db	4081	TATATATACAGACTCTTARTATGCTYACCTAGTCTNTCCATGCCCATGMRGCAATATGSAR	4140
QY	4141	AGAAAGGGAATTCCTTACTTCYAGRGAAACACCTATCAMACATCAGGAAGCCATTAGGAR	4200
Db	4141	AGAAAGGGAATTCCTTACTTCYAGRGAAACACCTATCAMACATCAGGAAGCCATTAGGAR	4200
QY	4201	ATTATTAYTGGCGTACAGAAACCTARAGAGGTGGMAGTCTTACACTGCYGGGTCATCA	4260
Db	4201	ATTATTAYTGGCGTACAGAAACCTARAGAGGTGGMAGTCTTACACTGCYGGGTCATCA	4260
QY	4261	NAAAGGAAGAAAGGGAATASAAAGGAAATGCGAAGCAKATATTGAAGCMAAAAGAGC	4320
Db	4261	NAAAGGAAGAAAGGGAATASAAAGGAAATGCGAAGCAKATATTGAAGCMAAAAGAGC	4320
QY	4321	TGCAAGGCGAGACCCCTCCATTAGAAATGCTTATTAACTTCCCTTAGTATAGGGTAATCC	4380
Db	4321	TGCAAGGCGAGACCCCTCCATTAGAAATGCTTATTAACTTCCCTTAGTATAGGGTAATCC	4380
QY	4381	CTTCCGGGAAACCAAGCCCGGTAGCTCAGCAGGAGAAACAGAAATGGGAACTTACCTGCAAC	4440
Db	4381	CTTCCGGGAAACCAAGCCCGGTAGCTCAGCAGGAGAAACAGAAATGGGAACTTACCTGCAAC	4440
QY	4441	CAGTTTCTCCCTCGGACGGTTAGCCACTGAAGAGGGAATACTTTTGCCTGCAAC	4500
Db	4441	CAGTTTCTCCCTCGGACGGTTAGCCACTGAAGAGGGAATACTTTTGCCTGCAAC	4500
QY	4501	TATCCAAATGGAATTAATTAACCCCTTATCAACCTTTTCACTTAGGCAATGATAGCAC	4560
Db	4501	TATCCAAATGGAATTAATTAACCCCTTATCAACCTTTTCACTTAGGCAATGATAGCAC	4560
QY	4561	CCATCARATGGCAATCAATTAATTTACTGGAACAGGCCCTTTTCAAACTATCAAGCARAT	4620
Db	4561	CCATCARATGGCAATCAATTAATTTACTGGAACAGGCCCTTTTCAAACTATCAAGCARAT	4620
QY	4621	AKTCAAGGCTGTGAATGTGCAARAAATATCCCTGCTYATCGCAAGCTCCTTC	4680
Db	4621	AKTCAAGGCTGTGAATGTGCAARAAATATCCCTGCTYATCGCAAGCTCCTTC	4680
QY	4681	AGGARAACAARAAACAGGCAATTTACCTGRABAACTGGCAACTGATTTTACCACAAG	4740
Db	4681	AGGARAACAARAAACAGGCAATTTACCTGRABAACTGGCAACTGATTTTACCACAAG	4740
QY	4741	CCCAACCTCAGGGATTTTCACTATCTAGTCTGGGTARATACCTTTCACGGTTGGCA	4800
Db	4741	CCCAACCTCAGGGATTTTCACTATCTAGTCTGGGTARATACCTTTCACGGTTGGCA	4800
QY	4801	PAGGCTTCCCTGTAGACAGAAAGGCCCAAGAGGTAATAAGGCACTAGTTTCAATGAA	4860
Db	4801	PAGGCTTCCCTGTAGACAGAAAGGCCCAAGAGGTAATAAGGCACTAGTTTCAATGAA	4860
QY	4861	ATAATTTCCAGATTCGGATTTCCCGAGGCTTACAGAGTGAATATAGCCCTGCTTCAG	4920
Db	4861	ATAATTTCCAGATTCGGATTTCCCGAGGCTTACAGAGTGAATATAGCCCTGCTTCAG	4920
QY	4921	GCCACAGTAACCCAGGAGTATCCAGGCGTTAGGTATACGATATCACTTACCTGCGCC	4980
Db	4921	GCCACAGTAACCCAGGAGTATCCAGGCGTTAGGTATACGATATCACTTACCTGCGCC	4980
QY	4981	TGAAGGCCACAGTCTCAGGGAAGGTGAGAAAAATGAATGAAAYACTCAAAAGGACATCTA	5040
Db	4981	TGAAGGCCACAGTCTCAGGGAAGGTGAGAAAAATGAATGAAAYACTCAAAAGGACATCTA	5040
QY	5041	AAAAAGCAACCCAGGAAACCCCACTCACTGCGCTGTCGTTGCTTATAGCCCTTAAA	5100
Db	5041	AAAAAGCAACCCAGGAAACCCCACTCACTGCGCTGTCGTTGCTTATAGCCCTTAAA	5100
QY	5101	AGAACTGCACTTTTCCCAAAAGCAGGCTTAGCCCATACGAAATGCTGTATGGAAGG	5160
Db	5101	AGAACTGCACTTTTCCCAAAAGCAGGCTTAGCCCATACGAAATGCTGTATGGAAGG	5160

QY	5161	CCCTTATACCAATGACCTTGTGCTTGACCCGAAGACAGCCAACTTAGTTGCGACATCA	5220
Db	5161	CCCTTATACCAATGACCTTGTGCTTGACCCGAAGACAGCCAACTTAGTTGCGACATCA	5220
QY	5221	CCTCCTTAGCCAAATCAACAGTTTCTTAAACATTTACAAGGAACCTTACCTCGAGAAG	5280
Db	5221	CCTCCTTAGCCAAATCAACAGTTTCTTAAACATTTACAAGGAACCTTACCTCGAGAAG	5280
QY	5281	AGGGAAGAACTATTTCACCCWGTGACATGCTATTAGTCAAGTCCCTTCYCTCTAATT	5340
Db	5281	AGGGAAGAACTATTTCACCCWGTGACATGCTATTAGTCAAGTCCCTTCYCTCTAATT	5340
QY	5341	CCCATCTCTAGATACATCTCGGAAGGACCTTACCCAGTCATTTTATYACCCCAACTG	5400
Db	5341	CCCATCTCTAGATACATCTCGGAAGGACCTTACCCAGTCATTTTATYACCCCAACTG	5400
QY	5401	CGGTTAAAGTGGCTGGAGTCTTGGATACATCACACTTGAGTCAAACTCTTGATAC	5460
Db	5401	CGGTTAAAGTGGCTGGAGTCTTGGATACATCACACTTGAGTCAAACTCTTGATAC	5460
QY	5461	TGCCAAGGAACCTGAAATTCAGGAGACAAAGCTAGCTATTCTGTGAACTCTAGAGG	5520
Db	5461	TGCCAAGGAACCTGAAATTCAGGAGACAAAGCTAGCTATTCTGTGAACTCTAGAGG	5520
QY	5521	ATTTGCGCTGCTCTTCAAAACAAACCAAGGAGGAAAGTAACTAAATCATAAATCCCC	5580
Db	5521	ATTTGCGCTGCTCTTCAAAACAAACCAAGGAGGAAAGTAACTAAATCATAAATCCCC	5580
QY	5581	ATGSSCCTCCCTTATCATATTTCTCTKTASTGTTTSTTTTACCTTCTTCTACTCTCCT	5640
Db	5581	ATGSSCCTCCCTTATCATATTTCTCTKTASTGTTTSTTTTACCTTCTTCTACTCTCCT	5640
QY	5641	GCACCCCTCCATGCGCTGTATGACCAAGTACCTCCCTYACCMAGAGTTTCTATGAGA	5700
Db	5641	GCACCCCTCCATGCGCTGTATGACCAAGTACCTCCCTYACCMAGAGTTTCTATGAGA	5700
QY	5701	ATGCAAGCTTCCCGGAAATTTTGTGCCCCCATCTGATAGAGTCTTTTSTAAGGGAACCCC	5760
Db	5701	ATGCAAGCTTCCCGGAAATTTTGTGCCCCCATCTGATAGAGTCTTTTSTAAGGGAACCCC	5760
QY	5761	ACCTTCACTGCCCCACACCATATATGCCCCCAACTGCTATCACTCTGCCACTCTTTGCAAG	5820
Db	5761	ACCTTCACTGCCCCACACCATATATGCCCCCAACTGCTATCACTCTGCCACTCTTTGCAAG	5820
QY	5821	CATGCAATATCTATTTATGACAGGAAATGATTAATCTAGTTGCTCTGAGGACTTT	5880
Db	5821	CATGCAATATCTATTTATGACAGGAAATGATTAATCTAGTTGCTCTGAGGACTTT	5880
QY	5881	GGAGTCACTGCTGCTGAGCTTACTTCAACCAACTGGTATGCTGATGGGGTGGAGTT	5940
Db	5881	GGAGTCACTGCTGCTGAGCTTACTTCAACCAACTGGTATGCTGATGGGGTGGAGTT	5940
QY	5941	CAAGATCAGGCAAGAGAAAAACATGTAAAAAGAGTAATCTCCAACTCACCGGGTACAT	6000
Db	5941	CAAGATCAGGCAAGAGAAAAACATGTAAAAAGAGTAATCTCCAACTCACCGGGTACAT	6000
QY	6001	GGCACTCTAGCCCCCTACAAAGGACTAGATCTCTCAAAAATACATGAAACCCCTCGTACC	6060
Db	6001	GGCACTCTAGCCCCCTACAAAGGACTAGATCTCTCAAAAATACATGAAACCCCTCGTACC	6060
QY	6061	CATCTCGCCTGGTAAAGCTTATTAACCACTCTGAGTCTGAGTCTGAGGCTCGGCC	6120
Db	6061	CATCTCGCCTGGTAAAGCTTATTAACCACTCTGAGTCTGAGTCTGAGGCTCGGCC	6120
QY	6121	CAAAAACCTACTAACTGTTGGATATGCTCCCTGAACTTCAAGCCATATGTTTCAATC	6180
Db	6121	CAAAAACCTACTAACTGTTGGATATGCTCCCTGAACTTCAAGCCATATGTTTCAATC	6180
QY	6181	CCTGTACTGAAACAAATGGAAACAACTTCAAGCAAGAAATAAACACCTTCCGTTTTAGTA	6240
Db	6181	CCTGTACTGAAACAAATGGAAACAACTTCAAGCAAGAAATAAACACCTTCCGTTTTAGTA	6240
QY	6241	GGACCTCTGTTTCCAAATSTGGAATAAACCCATACCTCAAAACCTCACCTGTGTAATAATTT	6300

LTR ORIGIN		Query Match Best Local Similarity 85.0%; Score 6448; DB 9; Length 10222; Matches 6681; Conservative 195; Mismatches 50; Indels 53; Gaps 27;	
QY	606	GATGGGAACGTTCCCGCAGACAAAGACGCGCTTAAGACGCTATTCTGGAATTTGGGA	665
DB	2886	GATGGGAACGTTCCCGCAGACAAAGACGCGCTTAAGACGCTATTCTGGAATTTGGGA	2945
QY	666	MCATTTTGACCTCAGACACTAAGAAAGAAACGACTTATATCTCTGCAAGTCCGCTG	725
DB	2946	CCATTTTGACCTCAGACACTAAGAAAGAAACGACTTATATCTCTGCAAGTCCGCTG	3005
QY	726	GCACCTCTGAGGAAGTATATAACCACTTCTACAGCTAGACCTTTCTTTGTAGAA	785
DB	3006	GCACCTCTGAGGAAGTATATAACCACTTCTACAGCTAGACCTTTCTTTGTAGAA	3065
QY	786	AAGGCAATGAGTGAAGTCCATAGTACAACTTTCTTTTCAATTAAGACAACTCAC	845
DB	3066	AAGGCAATGAGTGAAGTCCATAGTACAACTTTCTTTTCAATTAAGACAACTCAC	3125
QY	846	AATTATGTAAGAGTGTATTTATGCCCTACAGAAAGCCTTACAGTCTACCTCCCTATC	905
DB	3126	AATTATGTAAGAGTGTATTTATGCCCTACAGAAAGCCTTACAGTCTACCTCCCTATC	3185
QY	906	CCAGCATCCCGACTCTCTTCCCAATTAAGGACCCCTTCAACCCCAATGTCCAA	965
DB	3186	CCAGCATCCCGACTCTCTTCCCAATTAAGGACCCCTTCAACCCCAATGTCCAA	3245
QY	966	AAGGAGATAGACAAAGGGTAAACAGTGAACCAAGAGTGCCCAATATTCGCCAATATGA	1025
DB	3246	AAGGAGATAGACAAAGGGTAAACAGTGAACCAAGAGTGCCCAATATTCGCCAATATGA	3305
QY	1026	CCCTCCCAAGCAGTGGGAGAGAGAAATTCGSCCAGCAGAGTGCATGTGCTTTTXX	1085
DB	3306	CCCT--CCAGCAGTGGGAGAGAGAAATTCGSCCAGCAGAGTGCATGTGCTTTTTC	3364
QY	1086	TCTCCAGACTTAAAGCAATAAAGACAGACTTATAGTAAATCTCAGATAAATCTGATGG	1145
DB	3365	TCTCCAGACTTAAAGCAATAAAGACAGACTTATAGTAAATCTCAGATAAATCTGATGG	3424
QY	1146	CTATATTTGTTTAAAGGGTTAGACAATTTCTTTTGTATCTGACATGGAGAGATATATA	1205
DB	3425	CTATATTTGTTTAAAGGGTTAGACAATTTCTTTTGTATCTGACATGGAGAGATATA-A	3483
QY	1206	TGTCACTGTCTAATCAGACACTAACCCCAATCAGAGAGAGTGCCCAATATCTGACGCT	1265
DB	3484	TGTCACTGTCTAATCAGACACTAACCCCAATCAGAGAGAGTGCCCAATATCTGACGCT	3543
QY	1266	GAGGTGTTGGCGACTCTCTGATCTCAGTCAAGTCAATGGATANGGATGACAAACAGAGG	1325
DB	3544	GAGGTGTTGGCGACTCTCTGATCTCAGTCAAGTCAATGGATANGGATGACAAACAGAGG	3600
QY	1326	AAAGAAATGATTTCCCAACAGGCGAGCAGTCCAGTCTTASACCTCATTTGGGGAC	1385
DB	3601	AAAGAAATGATTTCCCAACAGGCGAGCAGTCCAGTCTTASACCTCATTTGGGG---	3657
QY	1386	ACAGAAATCAGTAACTAGGAGATTTGGTCTGACGACATTTGCTAATCTGTGTCTASAA	1445
DB	3658	ACAGAAATCAGAAACAT--GGAGATTTGGTCTGACGACATTTGCTAATCTGTGTCTAGAA	3716
QY	1446	GGACTAAGGAAACTAGGAAGAACTCTAGAAATTAATCAATGATGTCCACCAATACACA	1505

DB	3717	GGACTAAGGAAACTAGGAAG--AAGTCTATGAATTACTCAATGATGTCCACCAATAACACA	3775
QY	1506	GGGGAAGGAAGAAATCTCTACTGCTTCTTGAGAGAGACTAAGGAGGAGCAATTCAGGAAGC	1565
DB	3776	-GGGAAGGAAGAAATCTCTACTGCTTCTTGAGAGAGACTAAGGAGGAGCAATTCAGGAAGC	3834
QY	1566	GTGCTCTCTGTCACTGCTCTCTGGAAGGCCAACTAATCTTTAAAGCGTGAAGCTTTATCA	1625
DB	3835	GTGCTCTCTGTCACTGCTCTCTGGAAGGCCAACTAATCTTTAAAGCGTGAAGCTTTATCA	3894
QY	1626	CTCAGTCACTGCTGAGACATTTAG--AAAAAATTTCAAAAGTCTGCGTAGGCCCGGAGCAAA	1684
DB	3895	CTCAGTCACTGCTGAGACATTTAGAAAAAATTTCAAAAGTCTGCGTAGGCCCGGAGCAAA	3954
QY	1685	ACTTAAAGACCTTATTGAATTTGGCACTGCTGGTCTTTTATATAGAGATCAGAGAGAGC	1744
DB	3955	ACTTAAAGACCTTATTGAATTTGGCACTGCTGGTCTTTTATATAGAGATCAGAGAGAGC	4014
QY	1745	AGGCGGAACAGGACAAACGGGATTTAAAAAAGGCCACCGCTTTAGTCAATGACCTCAGG	1804
DB	4015	AGGCGGAACAGGACAAACGGGATTTAAAAAAGGCCACCGCTTTAGTCAATGACCTCAGG	4074
QY	1805	CAAGTGGACTTTGGAGGCTCTGGAAGGAAAGCTGGGCAAAATGAAATGCCCTAATAGG	1864
DB	4075	CAAGTGGACTTTGGAGGCTCTGGAAGGAAAGCTGGGCAAAATGAAATGCCCTAATAGG	4134
QY	1865	GCTTGGTCCAGTGGGCTCTACAGGACACTTTTAAAAAGATTTGTCCAGTAGAGTAAG	1924
DB	4135	GCTTGGTCCAGTGGGCTCTACAGGACACTTTTAAAAAGATTTGTCCAGTAGAGTAAG	4194
QY	1925	CGCCCTCTGCTCATGCCCTTATTTCAAGGGAATCACTGGAAGGCCCACTGCCCCAGG	1984
DB	4195	CGCCCTCTGCTCATGCCCTTATTTCAAGGGAATCACTGGAAGGCCCACTGCCCCAGG	4254
QY	1985	GGACAAAGGTCTTTTGAAGTCAAGGCACTAAACAGATGATCCAGCAGCAGGCTGAGGG	2044
DB	4255	GGACAAAGGTCTCTGAGTCAAGGCACTAAACAGATGATCCAGCAGCAGGCTGAGGG	4314
QY	2045	TGCTGGGCAAGCGGCATCCCATGCCATCACTCAGAGGCCCTGGGTATGCTTGACC	2104
DB	4315	TGCTGGGCAAGCGGCATCCCATGCCATCACTCAGAGGCCCTGGGTATGCTTGACC	4374
QY	2105	ATTGAGGGCCAGGAAGTGTCTCTGGAACACTGGTGGCTCTTCTTAGTCTTACTCTTC	2164
DB	4375	ATTGAGGGCCAGG--AGTGTGTCTCTGGAACACTGGTGGCTCTTCTTAGTCTTACTCTTC	4433
QY	2165	TGTCGGGCAACTGTCTCTCAGATCTGTCACTATTTCTGAGGGGGTCCNTAAGACGGGCA	2224
DB	4434	TGTCGGGCAACTGTCTCTCAGATCTGTCACTA-TCTGAGGGGGTCC--TAAGACGGGCA	4491
QY	2225	GTCACTAGATATCTTTTCCAGCCCAATAGTTATGAACTGGGAGGCTTTATTTCTTTCAC	2284
DB	4492	GTCACTAGATAT-TTCTCCAGCCCAATAGTTATG--ACTGGGGAGGCTTTATTTCTTTCAC	4549
QY	2285	ATGCTTTTCTAATATTGTTGAAAGCCCACTACCTTGTGTAGGAGAGACATTCAGCAA	2344
DB	4550	ATGCTTTTCTAATATTGTTGAAAGCCCACTACCTTGTGTAGGAGAGACATTCAGCAA	4609
QY	2345	AAGCAGGGGCCAATTATACCTGAAACATAGGAGAGGAAACACCCGTTTGTGTNCCCTG	2404
DB	4610	AAGCAGGGGCCAATTATACCTGAAACATAGGAGAGGAAACACCCGTTTGTGT-CCCTG	4668
QY	2405	CTTGAGGAAGGAATTAATCTGGAAGTCTGGGCAACAGAGGACATATGACGAGCAAA	2464
DB	4669	CTTGAGGAAGGAATTAATCTGGAAGTCTGGGCAACAGAGGACATATGACGAG-CAAA	4727
QY	2465	GAATCCCGTCTGTTCAAGTTAAATCAAGATTTCCACTCTCTTCCCTACCAAGGCA	2524
DB	4728	GAATCCCGTCTGTTCAAGTTAAATCAAGATTTCCACTCTCTTCCCTACCAAGGCA	4787
QY	2525	GTACCCCTCTCAGACCAAGGCCCAACAGGATTTCCAAAGATTTGTTAAGGACTTAAAGC	2584
DB	4788	GTACCCCTCTCAGACCAAGGCCCAACAGGACTCCAAAGATTTGTTAAGGACTTAAAGC	4847

Db	6976	AAACCTCAGGGAATTTTCAGTATCTACTAGTCTGGGTAGATACTTTCACGGGTGGGCGAGAG	7035
QY	4804	GCCTTCCCCTGTAGGACAGAAAGGCCCAAGAGGTAAATAAAGGCACCTAGTTTCATGAATA	4863
Db	7036	GCCTTCCCCTGTAGGACAGAAAGGCCCAAGAGGTAAATAAAGGCACCTAGTTTCATGAATA	7095
QY	4864	ATTCCACAGATTCGGACTTCCTCCGAGGCTTACAGAGTGACAAATAGCCCTGTTTCCAGGCC	4923
Db	7096	ATTCCACAGATTCGGACTTCCTCCGAGGCTTACAGAGTGACAAATAGCCCTGTTTCCAGGCC	7155
QY	4924	ACAGTAAACCCAGGGAGTATCCAGGCGTTAGGTATAGCATATCACTTACACTGGGCTGA	4983
Db	7156	ACAGTAAACCCAGGGAGTATCCAGGCGTTAGGTATAGCATATCACTTACACTGGGCTGA	7215
QY	4984	AGGCCACAGTCCTCAGGGAAGGTGAGAAAAATGAATGAAAYACATCAAAGGACATCTAAAA	5043
Db	7216	AGGCCACAGTCCTCAGGGAAGGTGAGAAAAATGAATGAAAYACATCAAAGGACATCTAAAA	7275
QY	5044	AAGCAAAACCCAGGAACCCACCTCACATGGCTGTTCTGTGGCTATAGGCTTAAAAAGA	5103
Db	7276	AAGCAAAACCCAGGAACCCACCTCACATGGCTGTTCTGTGGCTATAGGCTTAAAAAGA	7335
QY	5104	ATCTGCAACTTTCGCCAAAAGCAGGACTTAGCCCATACGAAATGCTGTATGGAAGGCC	5163
Db	7336	ATCTGCAACTTTCGCCAAAAGCAGGACTTAGCCCATACGAAATGCTGTATGGAAGGCC	7395
QY	5164	TTCTATAACCAATGACCTTGTCTTGACCCCAAGACAGCCAACTTAGTTGCAGACATCACCT	5223
Db	7396	TTCTATAACCAATGACCTTGTCTTGACCCCAAGACAGCCAACTTAGTTGCAGACATCACCT	7455
QY	5224	CTTTAGCCCAATATCAACAGTTCTTAAAAACATTAAGGAACCTATCCCTGAGAAAGG	5283
Db	7456	CTTTAGCCCAATATCAACAGTTCTTAAAAACATTAAGGAACCTATCCCTGAGAAAGG	7515
QY	5284	GAAGAAGAACTATTCCACCCWGTGACATGTTAGTCAAGTCCCTTCCTCTAAATCCC	5343
Db	7516	GAAGAAGAACTATTCCACCCWGTGACATGTTAGTCAAGTCCCTTCCTCTAAATCCC	7575
QY	5344	CATCCCTAGATACATCTCGGAAGGACCTTACCAGTCAATTTATYATACCCCACTGCGG	5403
Db	7576	CATCCCTAGATACATCTCGGAAGGACCTTACCAGTCAATTTATCTACCCCACTGCGG	7635
QY	5404	TTAAAGTGGCTGGAGTGGAGTCTTGGATACATCACACTTGAGTCAAACTCTGGATCTGC	5463
Db	7636	TTAAAGTGGCTGGAGTGGAGTCTTGGATACATCACACTTGAGTCAAACTCTGGATCTGC	7695
QY	5464	CAAAGGAACCTGAAAATCCAGGAGACAACCTAGCTATTCTCTGTAACCTCTAGAGGATT	5523
Db	7696	CAAAGGAACCTGAAAATCCAGGAGACAACCTAGCTATTCTCTGTAACCTCTAGAGGATT	7755
QY	5524	TGGCCCTGCTCTTCAAAACAAACAGGAGGAAGTAACATAAAATCATAAATCCCCCATG	5583
Db	7756	TGGCCCTGCTCTTCAAAACAAACAGGAGGAAGTAACATAAAATCATAAATCCCCCATG	7814
QY	5584	GSCTCCCTTATCATATTTTCTCTKTATGTTTAAACCTTCTCTCATCTCATCTGCA	5643
Db	7815	GSCTCCCTTATCATATTTTCTCTKTATGTTTAAACCTTCTCTCATCTCATCTGCA	7874
QY	5644	CCCCCTCCATGCGCTGTATGACAGTAGCTCCCTTACCMAGAGTTTCTATGGGAATG	5703
Db	7875	CCCCCTCCATGCGCTGTATGACAGTAGCTCCCTTACCMAGAGTTTCTATGGGAATG	7934
QY	5704	CAGGCTCCCGGAATATTTGATGCCCATCGTATAGGAGTCTTTSTAAGGAACCCCCACC	5763
Db	7935	CAGGCTCCCGGAATATTTGATGCCCATCGTATAGGAGTCTTTSTAAGGAACCCCCACC	7994
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LOCUS Homo sapiens isolate 79 endogenous retrovirus HERV-W, ERVWE1 locus,
DEFINITION allele B, complete sequence.
ACCESSION AY101585
VERSION AY101585.1 GI:37544405
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10222)
AUTHORS Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
TITLE The endogenous retroviral locus ERVWE1 is a bona fide gene involved
in hominoid placental physiology
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
PUBMED 14757826
REFERENCE 2 (bases 1 to 10222)
AUTHORS Mallet,F., Bouton,O. and Oriol,G.
TITLE Direct Submission
JOURNAL Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
CNRS-bioMerieux, Ecole Normale Supérieure de Lyon - 46 allée
d'Italie, Lyon 69364 cedex 07, France
FEATURES
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VERSION AX329572.1 GI:18102550
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ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
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REFERENCE
AUTHORS Young, P. E., Augustus, M., Carter, K. C., Ebner, R., Endress, G.,
Horriqan, S., Soppet, D. R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic(C) screening using signature
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JOURNAL Patent: WO 0194629-A 84 13-DEC-2001;
Avalon Pharmaceuticals (US)
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RESULT 9
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LOCUS AC007566 149194 bp DNA linear PRI 01-MAR-2002
DEFINITION Homo sapiens BAC clone CTB-10G5 from 7q21-7q22, complete sequence.
ACCESSION AC007566
VERSION AC007566.2 GI:11181861
KEYWORDS HTG.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 149194)
Sulston, J.E. and Waterston, R.
Toward a complete human genome sequence
Genome Res. 8 (11), 1097-1108 (1998)
99063792
9847074

REFERENCE 2 (bases 1 to 149194)
AUTHORS Du, Z.
TITLE The sequence of Homo sapiens BAC clone CTB-10G5
JOURNAL Unpublished (2001)
3 (bases 1 to 149194)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (15-MAY-1999) Genome Sequencing Center, Washington
MO 63108, USA
4 (bases 1 to 149194)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (02-OCT-2000) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
5 (bases 1 to 149194)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
6 (bases 1 to 149194)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JAN-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
7 (bases 1 to 149194)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (06-FEB-2002) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
8 (bases 1 to 149194)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Nov 16, 2000 this sequence version replaced gi:4835815.

COMMENT
----- Genome Center
Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc>
Contact: sapinsew@wustl.edu
----- Summary Statistics

Center project name: H_RG010G05

NOTICE: This sequence may not represent the entire insert of this

clone. It may be shorter because we only sequence overlapping
clone sections once, or longer because we provide a small overlap
between neighboring data submissions.

This sequence was finished as follows unless otherwise noted:
all regions were double stranded, sequenced with an alternate
chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such
as compressions and repeats; all regions were covered by sequence
from more than one subclone; and the assembly was confirmed by
restriction digest.

MAPPING INFORMATION:

The sequence of this clone was established as part of a mapping and
sequencing collaboration between the NHGRI McPherson 7 Mapping
Project (Eric D. Green, Director), John D. McPherson in the
Department of Genetics (Washington University), and the Washington
University Genome Sequencing Center. For additional information
about the map position of this sequence, see
<http://www.nhgri.nih.gov/DIR/CTB/CHR7>, send
<mailto:egreen@nhgri.nih.gov>, or see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

Clone CTB-10G5 is from the first release of the human BAC library
CTB-978SK-B. The library contains cloned DNA from the male
fibroblast cell line 978SK. See: Shizuya et al., Proc. Natl. Acad.
Sci. USA 89:8794-7 (1992); U-J. Kim et al., Genomics 34:213-8
(1996). This clone is available from Research Genetics, Inc.
(<http://www.resgen.com>).
VECTOR: pBelOBAcl1
Selection: chloramphenicol

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the left is RP5-911H5, 200 base pair
overlap. Actual start of this clone is at base position 195 of
CTB-10G5; actual end is at base position 150532 of CTB-10G5.

The clone CTB-10G5 contains the entire sequence of CTB-83M5.

FEATURES

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Query Match 85.0%; Score 6448; DB 9; Length 149194;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 6681; Conservative 195; Mismatches 50; Indels 53; Gaps 27;
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Qy	2405	CTTGAGGAAGGAATTAATCTCTGAAGTCTGGGCAACAGAGACAATATGACAGCAGCAAA	2464
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Db	89209	GAATGCCGCTCTGTTCAAGTTAACTAAAGGATTCACCTTCTTCCCTACCAAGGCA	89150
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Qy	2705	CGTTGTCTTTTATACCCAGCTGTACTAGCCCTTATCTGTGMYTTCACAAATACCAGA	2764
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Qy	2765	GGAGCAGAGTGGTTTACATCTCTGGACCTTMAAGTGCCTTCTCTGCACTCCCTGTACA	2824
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Qy	2825	TCCTGACTCTCAATCTTGTGTTGCTTTGAAAGATCTTCAAAACCCACATCTCAACTCAC	2884
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Qy	2885	CTGGACTTTTACCCAAAGGGTTACGGGATAGYCCCCATCTATTTTGGCCAGGCATTAGC	2944
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Db	88738	CCAAGACTTGAGCAATCTCTATACCTGGACA--CTTGTCTCTCGGTAGGTGATGATTT	88681
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Qy	3065	CCTCGCVACCTGTGGCTCAWGGTTTCAAACASARAGCTCARCTCTGTCTCACAGCAGGT	3124
Db	88620	CCTCGCTACTCTGTGGCTACATGGTTTCAAACCAAGGCTCAACTCTGTCTCACAGCAGGT	88561
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Db	88444	AATAGTCTTCTGCGCAAAATGGATT-CCCAGGTATGCGCAAAATAGCCAGGTCAATAATA	88386
Qy	3305	CASTAATAAGGAACTCAGAAAGCAATAACCATTTATPAAGATGGAAYMTGAAGYMR	3364
Db	88385	CACATAAAGGAACTCAGAAAGCAATAACCATTTATAGTAAGATGACAACTGAAGTAG	88326
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Db	88325	AAGTGGCTTCCAGGCC-----TAAACCCAGGCCAGTGTGAAGTGTGGCC	88280
Qy	3425	AACRGGGCAAGACTTTTSTTYATYRTCAAGAAAAAACAAGAAVAGCTCTRGGAGTCC	3484
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Qy	3485	TTACACAGTCTCAGGAGYAGCTTGCACCCYRTGCRYACCTGAATGAAGAAAYTGAATG	3544
Db	88220	TTACACAGATCCAGGAGTGCAGCTTGCACCTGTGCACTACCTGACCTAAGGAAATGATG	88161
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Db	88160	TAGTGGCAAGGGTGTGCACTTGTGTTTACGGGTAGTGGTGGCAGTAGCTVKTAGTAT	88101
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QY	4025	GCAGAACTAATAGCCYCAVTKGGGCACTAGAAATTTAGGAGAAAGAAAGGYYAAATATA	4084	Db	86601	ATCTGCAACTTTCCCAAAAAGCAGGACTTAGCCCATACGAAATGCTGTATGGAAGGCC	86542
Db	87681	GCAGAACTAATAGCCYCAVTKGGGCACTAGAAATTTAGGAGAAAGAAAGGYYAAATATA	87622	QY	5164	TTCAATACCAATGACCTTTGCTTGACCCCAAGACGCGCAACTTAGTTGCGAGACATCACT	5223
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Db	87621	TATACAGACTCTTAAATATGCTTACCTAGTCTTCCATGAGGCAATATGAGAAATATA	87562	QY	5224	CTTTAGCCCAATATCAACAAAGTTCTTAAACATTTCAAGGAACCTATCCCTGAGAGAGG	5283
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QY	4265	GGAAAGGAAAGGGAATATSAAGGAAATGCGCAAGCAKATATTTGAAGGMAAAAGAGCTGCA	4324	Db	86361	CATCCCTAGATACATCCTGGGAGGACCTTACCAGTCAATTTATTTATACCCCAACTGCGG	86302
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RESULT 10
LOCUS   AY101583              10222 bp      DNA      linear      PRI 11-FEB-2004
DEFINITION Homo sapiens isolate 21 endogenous retrovirus HERV-W, ERVWE1 locus, allele B, complete sequence.
ACCESSION AY101583
VERSION   AY101583.1 GI:37544401
KEYWORDS  .
SOURCE    Homo sapiens (human)
ORGANISM  Homo sapiens
REFERENCE 1 (bases 1 to 10222)
AUTHORS   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Mallet,F., Bouton,O., Prudhomme,S., Cheynet,V., Oriol,G.,
Bonnaud,B., Lucotte,G., Duret,L. and Mandrand,B.
The endogenous retroviral locus ERVWE1 is a bona fide gene involved
in hominoid placental physiology
Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)
JOURNAL   14757826
PUBMED    14757826
REFERENCE 2 (bases 1 to 10222)
AUTHORS   Mallet,F., Bouton,O. and Oriol,G.
DIRECT SUBMISSION
TITLE      Submitted (06-MAY-2002) Retrovirology Department, UMR 2142
JOURNAL   CNRS-bioMerieux, Ecole Normale Supérieure de Lyon - 46 allée
d'Italie, Lyon 69364 cedex 07, France
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9487. .10222
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LTR
ORIGIN

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Query Match      85.0%; Score 6446.4; DB 9; Length 10222;
Best local Similarity 95.7%; Pred. No. 0;
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[illegible]

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LOCUS BD221808 10499 bp DNA linear PAT 17-JUL-2003
DEFINITION Nucleic sequence and deduced protein sequence family with human
endogenous retroviral motifs, and their uses.
ACCESSION BD221808
VERSION BD221808.1 GI:33031578
KEYWORDS JP 2002518051-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 10499)
AUTHORS Alliel,P.M., Perin,J.P. and Rieger,F.
TITLE Nucleic sequence and deduced protein sequence family with human
endogenous retroviral motifs, and their uses
JOURNAL Patent: JP 2002518051-A 3 25-JUN-2002;
INSTITUT NATIONAL DE LA SANTE ET DE LA RECHERCHE MEDICALE
COMMENT OS Homo sapiens (human)
PN JP 2002518051-A/3
PD 25-JUN-2002
PF 23-JUN-1999 JP 2000556036
PR 23-JUN-1998 FR 98/07920
PI PATRICK M ALLIEL, JEAN PIERRE PERIN, FRANCOIS RIEGER PC
C12N15/09, A01K67/027, A61K31/711, A61K48/00, A61P21/00, PC
A61P25/00.
PC A61P37/06, C07K14/15, C12Q1/68, C12Q1/70, C12N15/00 CC Nucleic
sequence and deduced protein sequence family with CC
human endogenous
CC retroviral motifs, and their uses
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DEFINITION	Pan troglodytes isolate 1 endogenous retrovirus ERV-W, ERVW1 locus, allele A, complete sequence.	
ACCESSION	AY101586	
VERSION	AY101586.1 GI:37544407	
KEYWORDS		
SOURCE	Pan troglodytes (chimpanzee)	
ORGANISM	Pan troglodytes	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.	
AUTHORS	Mallet, F., Bouton, O., Prudhomme, S., Cheynet, V., Oriol, G., Bonnaud, B., Lucotte, G., Duret, L., and Mandrand, B.	
TITLE	The endogenous retroviral locus ERVW1 is a <i>Dona fide</i> gene involved in hominoid placental physiology	
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 101 (6), 1731-1736 (2004)	
PUBMED	14757826	
REFERENCE	2 (bases 1 to 10229)	
AUTHORS	Mallet, F., Bouton, O. and Oriol, G.	
TITLE	Direct Submission	
JOURNAL	Submitted (06-MAY-2002) Retrovirology Department, UMR 2142 CNRS-bioMerieux, Ecole Normale Supérieure de Lyon - 46 allée d'Italie, Lyon 69364 cedex 07, France	
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ORIGIN		
Query Match	83.7%; Score 6346.4; DB 9; Length 10229;	
Best Local Similarity	94.9%; Pred. No. 0;	
Matches 6625; Conservative 194; Mismatches 110; Indels 52; Gaps 28;		
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Db	8900	TCGCGCACTCCCTGGTCACTTGCAGATCAACTTAATCCCTAGCAGCAGTAGTCTCTTC	8959
QY	6722	RAAATCGAAGAGCTTTAGACTGCTAACCGCTGAGAGAGGGGAACTGTTTATTTTATAG	6781
Db	8960	RAAATCGAAGAGCTTTAGACTGCTAACCGCTGAGAGAGGGGAACTGTTTATTTTATAG	9019
QY	6782	GGGAGGATCTGTTATTTATTTATTAATCAATCCGGAATCGTCACTGAGAAAGTTTAAAGAA	6841
Db	9020	GGGAGGATCTGTTATTTATTTATTTATTAATCAATCCGGAATCGTCACTGAGAAAGTTTAAAGAA	9079
QY	6842	TTCSAGATCGAATAACAGTACAGCAGAGAGCTTCGAAACACTTGGACCTCGGGGCTCC	6901
Db	9080	TTCSAGATCGAATAACAGTACAGCAGAGAGCTTCGAAACACTTGGACCTCGGGGCTCC	9139
QY	6902	TCAGCCCATGAGATCCCTGGATTTCTCCCTTTAGGACCTCTAGCAGCTATATATTCG	6961
Db	9140	TCAGCCCATGAGATCCCTGGATTTCTCCCTTTAGGACCTCTAGCAGCTATATATTCG	9199
QY	6962	TACTCTCTTTGGACCTGTATCTTTACCTCTTGTACTTTGTCTCTTCCAGAAATCG	7021
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QY	7022	AAGCTGTAAACTCAAAATGAGCCCAAGATGCAAGTCCAGACTTAAAGATCTACCGCAGAC	7081
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QY	7082	CCCTGGACCGGCTCTGTAGCCCAAGATCTGTAGTAAATGAATCAAAAGGCACTCTCTG	7141
Db	9320	CCCTGGACCGGCTCTGTAGCCCAAGATCTGTAGTAAATGAATCAAAAGGCACTCTCTG	9379
QY	7142	AGGAAATCTAGCTGACAACTCTACTACGCCCAATTCACGAGGAGCAGTAGTAGCG	7201
Db	9380	AGGAAATCTTAACTGACAACTCTACTACGCCCAATTCACGAGGAGCAGTAGTAGCG	9439
QY	7202	GTSGTCGCGCACTCCCAACAGCACTTAGTCTTCTGTTGAGATGGGCACTGAGAG	7261
Db	9440	GTSGTCGCGCACTCCCAACAGCACTTAGTCTTCTGTTGAGATGGGCACTGAGAG	9499
QY	7262	ACAGGACTAGCTGGATTTCTTAGGCTGATTAAGAAATCCCTAGCTAGTGGGAGGTGA	7321
Db	9500	ACAGGACTAGCTGGATTTCTTAGGCTGATTAAGAAATCCCTAGCTAGTGGGAGGTGA	9559
QY	7322	CCACATCCACCTTTTAAACACCGGGCTTGCACCTTAGTTCACACCTGACCAATCAGAGGC	7381
Db	9560	CCACATCCACCTTTTAAACACCGGGCTTGCACCTTAGTTCACACCTGACCAATCAGAGGC	9619
QY	7382	TCACCTAAATATCTAATAGGCAAGACAGGAGGTAAGAAATAGCAATCATTTATTGCM	7441
Db	9620	TCACCTAAATATCTAATAGGCAAGACAGGAGGTAAGAAATAGCAATCATTTATTGCC	9679
QY	7442	TCAGAGCACAGCAGGAGGACAAATGATCGGATATATAAACCAGTCTTCGAGCGGCAAC	7501
Db	9680	TCAGAGCACAGCAGGAGGACAAATGATCGGATATATAAACCAGTCTTCGAGCGGCAAC	9739
QY	7502	GGCAACCCCTTTGGTCCCTTCTGATGGAGCTCTCTTTTCATGCTATTTCAT	7561
Db	9740	GGCAACCCCTTTGGTCCCTTCTGATGGAGCTCTCTTTTCATGCTATTTCAT	9799
QY	7562	CTATTAAATCTTGCACCTGCR	7582
Db	9800	CTATTAAATCTTGCACCTGCA	9820
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LTR
ORIGIN

Query Match 83.7%; Score 6344.8; DB 9; Length 10229;
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QY	666	MCATTTGACCTCAGACACTAAGAAAGAAACGACTTATATTTCTGAGTGCGCCCTG	725
DB	2948	CCAAATTTGACCTCAGACACTAAGAAAGAAACGACTTATATTTCTGAGTGCGCCCTG	3007
QY	726	GCACCTCAGGGAAGTATAAATTATAACACATCTTACAGCTAGACCTTTTGTAGAA	785
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QY	906	CCAGCATCCCC--GACTCTCTCCCAATTAAGACAGCCCTTCAACCCAAATGGTCC	963
DB	3188	CCAGCATCCCCGACTCTCTCCCAATTAAGACAGCCCTTCAACCCAAATGGTCC	3247
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DB	3248	AAAAGGAGATAGACAAAAGGGTAAACAGTGAAACCAAGAGTGCCTAATATCCCAATAT	3307
QY	1024	GAACCTCCCAAGCAGTGGAGGAGAGAAATTCGGCCCAAGCAGAGTGCATGTCYTTTT	1083
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QY	1084	YVTCCTCCAGACTTAAAGCAATATAAACAAGACTTAGTAAATTCAGATTAATCTGAT	1143
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QY	1324	GGAAAGANAATGATTTCCCAAGGCAGCAGCAGTCTCCAGTCTASACCTCATTTGGG	1383
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QY	1564	GGGTGCTCTCTGTCACTGACTCTTCTCAAGGCAACTAACTTAAAGCGTAAAGTTTAT	1623
DB	3837	GGGTGCTCTCTGTCACTGACTCTTCTCAAGGCAACTAACTTAAAGCGTAAAGTTTAT	3896
QY	1624	CACTAGTCAGCTGAGACATTTAG--AAAAAATTCAAAAGTCTGCGTAGGCCCGGAGCA	1682
DB	3897	CACTAGTCAGCTGAGACATTTAGAAAAAACTTCAAAAGTCTGCGTAGGCCCGGAGCA	3956
QY	1683	AAACTTTAGAAACCTTATTTGAACTTGGCACTCTGGTCTTTTATTAATAGAGATCAGAGGA	1742
DB	3957	AAACTTTAGAAACCTTATTTGAACTTGGCTACCTCGGTTTTTATTAATAGAGATCAGAGGA	4016
QY	1743	GCAGCGGAAACAGGACAAACGGGATTTAAAAAAGGCCACCGCTTTAGTCATGACCTCA	1802
DB	4017	GCAGCGGAAACAGGACAAACGGGATTTAAAAAAGGCCACCGCTTTAGTCATGACCTCA	4076
QY	1803	GGCAAGTGAATTTTGGAGGCTCTGAAAAAGGAAAGCTGGCAAAATTTGAATGCCCTAATA	1862
DB	4077	GGCAAGTGAATTTTGGAGGCTCTGAAAAAGGAAAGCTGGCAAAATTTGAATGCCCTAATA	4136
QY	1863	GGGCTTGTCTCAGTGCGGCTCTACAGGACACTTTAAAAAAGATTGTCCAAGTAGAGTA	1922
DB	4137	GGGCTTGTCTCAGTGCGGCTCTACAGGACACTTTAAAAAAGATTGTCCAAGTAGAGTA	4196
QY	1923	AGCGGCTTGTCTGCTCCATGCGGCTTTATTTCAAGGAAATCACTGGAAGGCCACTTGCCCCA	1982
DB	4197	AGCGGCTTGTCTGCTCCATGCGGCTTTATTTCAAGGAAATCACTGGAAGGCCACTTGCCCCA	4256
QY	1983	GGGGAACAAAGGTCTTTTGTAGTCAAGACCACTTAACAGATGATCCAGCAGCAGGACTGAG	2042
DB	4257	GGGGAACAAAGGTCTCTGAGTCAGAAAGCCTTAACAGATGATCCAGCAGCAGGACTGAG	4316
QY	2043	GCTGCTGGGCAAGCGGCTCCCATGCGCTACACCTCAGAGAGCCCTGGGTATGCTTCA	2102
DB	4317	GCTGCTGGGCAAGCGGCTCCCATGCGCTACACCTCAGAGAGCCCTGGGTATGCTTCA	4376
QY	2103	CAATGAGGGCCAGGAAGTTGTCTCTGAGACACTGCTGCGGTCTTTTAGTCTTACTCT	2162
DB	4377	CAATGAGGGCCAGG--AGTTTGTCTCTGAGACACTGCTGCGGTCTTTTAGTCTTACTCT	4435
QY	2163	TCTGTCCGGAACAATGCTCTCCAGATCTGTCACTA--TCTGAGGGGGTCC--TAAGACAGG	2222
DB	4436	TCTGTCCGGAACAATGCTCTCCAGATCTGTCACTA--TCTGAGGGGGTCC--TAAGACAGG	4493
QY	2223	CAGTCACATAGATATCTTCTCCAGGCTAAGTTATGAATGAGGAGCTTTATCTTTTC	2282
DB	4494	CAGTCACATAGATATCTTCTCCAGGCTAAGTTATGAATGAGGAGCTTTATCTTTTC	4551
QY	2283	ACATGCTTTTCTAATATGCTTGAAGCCCACTACCTTGTAGGAGAGACATTTCTAGC	2342
DB	4552	ACATGCTTTTCTAATATGCTTGAAGCCCACTACCTTGTAGGAGAGACATTTCTAGC	4611
QY	2343	AAAAGCGGGGCCATTTATACCTTGAAATAGGAGAAAGAAACAACCGTTTGTGTGNC	2402
DB	4612	AAAAGCGGGGCCATTTATACCTTGAAATAGGAGAAAGAAACAACCGTTTGTGTGNC	4670
QY	2403	TGCTTGGAGGAAGAAATTAATCCTCAAGTCTGGGCAACAGAGGACAAATATGACAGGCA	2462
DB	4671	TGCTTGGAGGAAGAAATTAATCCTCAAGTCTGGGCAACAGAGGACAAATATGACAGGCA	4729
QY	2463	AAGAAATGCCCTCTGTTTCAAGTTAAATTAAGGATTCACCTCTCTTCCCTACCAAGG	2522
DB	4730	AAGAAATGCCCTCTGTTTCAAGTTAAATTAAGGATTCACCTCTCTTCCCTACCAAGG	4789
QY	2523	CAGTACCCCTCTCAGACCCCAAGGCCCAACAGAGTTCCAAAGATTGTTAAGGACTTAAAA	2582
DB	4790	CAGTACCCCTCTCAGACCCCAAGGCCCAACAGAGTTCCAAAGATTGTTAAGGACTTAAAA	4849

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Db	7042	AGGCTTCCCTCTAGGACAGAAAAGGCCCAAGAGTAAATAAGSCATCTACTCATGAAA	7101
Qy	4862	TAAATCCAGATTCGGACTTCCCGAGGCTTTCAGAGTGAACAATAGCCCTCTTTCCAGG	4921
Db	7102	TAAATCCAGATTCGGACTTCCCGAGGCTTTCAGAGTGAACAATAGCCCTCTTTCCAGG	7161
Qy	4922	CCAGTAAACCCAGGAGTATCCAGGCGTTAGGTATACGATATCACTTACACTGCGCT	4981
Db	7162	CCAGTAAACCCAGGAGTATCCAGGCGTTAGGTATACGATATCACTTACACTGCGCT	7221
Qy	4982	GAAGGCCACAGTCTCAGGGAAGTTCGAGAAAATGAATGAAYACTCAAGAGCATCTAA	5041
Db	7222	GAAGGCCACAGTCTCAGGGAAGTTCGAGAAAATGAATGAAYACTCAAGAGCATCTAA	7281
Qy	5042	AAAAAGCAAAACCCAGGAAAACCCACTCTCAATGGCCCTGYTCTGTTCCTATAGCCCTTAAAAA	5101
Db	7282	AAAAAGCAAAACCCAGGAAAACCCACTCTCAATGGCCCTGYTCTGTTCCTATAGCCCTTAAAAA	7341
Qy	5102	GAATCTGCAACTTTCCCAAAAAGCAGGACTTAGCCCATACGAAATGCTGTATGGAAGGC	5161
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Qy	5162	CCTTCATAACCAATGACTTGTGTCTGACCCCAAGCAGGCAACTTAGTTCGAGACATCAC	5221
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Qy	5222	CTCCTTAGCCAAATPATCAACAAGTTCTTAAACAATTACAAGGAACCTATCCCTGAGAAGA	5281
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Qy	5282	GGGAAAAGAACTATTCCACCCTTGTGATGATGATGATGATGATGATGATGATGATGATG	5341
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Qy	5342	CCATCCCTAGATACATCTCGGGAAGGACCTACCCAGTCACTTTATATATATATATATAT	5401
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Qy	5522	TTTGGCGCTGCTCTTCAAAACAAACAGGAGGAAAGTAACTAAATCATAAATCCCCCA	5581
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Qy	6182	CTGTACTGAAATGGAACAACTTCAGCAAGAAATPAAACACCACTTCCTCGTTCCTAG	6241
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Qy	6482	CTGAAACAAGATTTATACAGTTATGTCTATCTAAGCCCCGCAACAAAGAGTACCCATTC	6541
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Qy	6602	CAACCTCTACTCAGTTTCTACTACAACTATCTCAAGAACTAAATGGGACATGGACGGG	6661
Db	8840	CAACCTCTACTCAGTTTCTACTACAACTATCTCAAGAACTAAATGGGACATGGACGGG	8899
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Qy	6722	RAAATCGAAGAGCTTTAGACTGCTAAACCGCTGAGAGAGGGGAACTGTTTATTTTAG	6781
Db	8960	RAAATCGAAGAGCTTTAGACTGCTAAACCGCTGAGAGAGGGGAACTGTTTATTTTAG	9019
Qy	6782	GGGAAAGTCTGTTTATTTATGTTTAACTCAATCCGGAATCGTCACTGAGAAAGTTAAAGAA	6841
Db	9020	GGGAAAGTCTGTTTATTTATGTTTAACTCAATCCGGAATCGTCACTGAGAAAGTTAAAGAA	9079
Qy	6842	TTCSAGATCGAATACAACTAGAGCAGAGAGCTTCGAAACACTGGACCTCGGGCTCC	6901
Db	9080	TTCSAGATCGAATACAACTAGAGCAGAGAGCTTCGAAACACTGGACCTCGGGCTCC	9139
Qy	6902	TCAGCCATGAGTGCCTGGAATCTCCCTTTCTTAGGACTCTAGCAGCTATATATTC	6961
Db	9140	TCAGCCATGAGTGCCTGGAATCTCCCTTTCTTAGGACTCTAGCAGCTATATATTC	9199

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: November 15, 2005, 21:00:58 ; Search time 1110 Seconds
(without alignments)
11176.802 Million cell updates/sec

Title: US-10-717-580-11
Perfect score: 7582
Sequence: 1 caacaatcggtataataacc.....tattaatcttgcarctgcr 7582

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	6124.6	80.8	8523	4	US-09-573-080A-21
C	2994.2	39.5	77772	4	US-09-949-016-17417
C	2994.2	39.5	77997	4	US-09-949-016-12249
5	2888.6	38.1	2946	3	US-09-175-928-3
C	2615.4	34.5	168394	4	US-09-949-016-13002
C	2220.4	29.3	145320	4	US-09-949-016-15858
8	2204	29.1	2763	4	US-09-949-016-5640
9	2168	28.6	8399	4	US-09-573-080A-26
10	1837.4	24.2	2304	4	US-08-979-847B-87
11	1507.4	19.9	276687	4	US-09-949-016-13940
12	1452.4	19.2	2364	4	US-08-979-847B-88
13	1415.8	18.7	2391	3	US-08-691-563C-57
14	1415.8	18.7	2391	4	US-08-374-766-57
15	1415.8	18.7	2391	4	US-08-979-847B-53
16	1341.8	17.7	8919	4	US-09-573-080A-54
17	1324.2	17.5	1481	4	US-08-979-847B-105
18	1312.4	17.3	1600	4	US-08-979-847B-207
19	1301.8	17.2	1600	4	US-08-979-847B-206
20	1282.4	16.9	1897	4	US-08-979-847B-205
21	1200.2	15.8	3910	3	US-09-120-653D-1
22	1089.2	14.3	1511	4	US-08-979-847B-117
23	1069.4	14.1	1577	3	US-08-691-563C-89
24	1069.4	14.1	1577	4	US-09-374-766-89
25	1069.4	14.1	1577	4	US-08-979-847B-83
26	996.8	13.1	2330	3	US-09-120-653D-4
27	947.8	12.5	1167	3	US-08-691-563C-61

28	947.8	12.5	1167	4	US-09-374-766-61	Sequence 61, Appl
29	947.8	12.5	1167	4	US-08-979-847B-57	Sequence 57, Appl
30	932.4	12.3	1158	1	US-08-471-724-1	Sequence 1, Appl
31	932.4	12.3	1158	2	US-08-471-724-1	Sequence 1, Appl
32	932.4	12.3	1158	2	US-08-384-137-1	Sequence 1, Appl
33	932.4	12.3	1158	2	US-08-470-006A-1	Sequence 1, Appl
34	932.4	12.3	1158	3	US-08-691-563C-1	Sequence 1, Appl
35	932.4	12.3	1158	3	US-09-200-990-1	Sequence 1, Appl
36	932.4	12.3	1158	3	US-09-133-411-1	Sequence 1, Appl
37	932.4	12.3	1158	4	US-09-374-766-1	Sequence 1, Appl
38	914	12.1	99580	4	US-08-979-847B-1	Sequence 1, Appl
C	895	11.8	68778	4	US-09-949-016-17411	Sequence 17411, A
C	863.4	11.4	149971	4	US-09-949-016-16406	Sequence 16406, A
C	784	10.3	42917	4	US-09-949-016-13590	Sequence 13590, A
42	722.6	9.5	1329	4	US-08-979-847B-108	Sequence 108, App
43	644.4	8.5	2448	3	US-08-691-563C-53	Sequence 53, Appl
45	644.4	8.5	2448	4	US-09-374-766-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-09-949-016-17382
; Sequence 17382, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17382
; LENGTH: 13537
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-17382

Query Match	85.0%	Score 6448;	DB 4;	Length 13537;
Best Local Similarity	95.7%	Pred. No. 0;		
Matches 6681;	Conservative 195;	Mismatches 50;	Indels 53;	Gaps 27;
QY	606	GATGGAAACGTTCCCGCAAGACAAACGCGCCCTTAAGACGCTATTCTTGGAAATTTGGGA	665	
DB	4610	GATGGAAACGTTCCCGCAAGACAAACGCGCCCTTAAGACGCTATTCTTGGAAATTTGGGA	4669	
QY	666	MCAATTTGACCTCAGACACTAAGAAAGAAAGCACTATATTTCTTCGAGTCCCGCTG	725	
DB	4670	CAATTTGACCTCAGACACTAAGAAAGAAAGCACTATATTTCTTCGAGTCCCGCTG	4729	
QY	725	GCACCTCTGAGGGAAGTATAAATTAACACCATCTTACAGCTAGACACTTTTGTAGAA	785	
DB	4730	GCACCTCTGAGGGAAGTATAAATTAACACCATCTTACAGCTAGACACTTTTGTAGAA	4789	
QY	786	AAGGCAATGGAGTGAAGTGCATTAAGTACAACTTTCTTTTCAATTAAGAGACAACTCAC	845	
DB	4790	AAGGCAATGGAGTGAAGTGCATTAAGTACAACTTTCTTTTCAATTAAGAGACAACTCAC	4849	
QY	846	RAATATGTAAGAGTGTGATTTATCCCTTACAGGAGCCCTCAGAGTCTACCTCCCTATC	905	
DB	4850	RAATATGTAAGAGTGTGATTTATCCCTTACAGGAGCCCTCAGAGTCTACCTCCCTATC	4909	
QY	906	CCAGCATCCCGACTCTTCTCCCAATTAATAGGACCCCTTCAACCAATGGTCCAA	965	

QY 7504 CAACCCCTTTGGGTCCTCCCTTTGATGGAGCTCTGTTTTCATGCTATTTCACTCT 7563
DB 11459 CAACCCCTTTGGGTCCTCCCTTTGATGGAGCTCTGTTTTCATGCTATTTCACTCT 11518

QY 7564 ATTAATCTTGCARTGCR 7582
DB 11519 ATTAATCTTGCARTGCA 11537

RESULT 2
US-09-573-080A-21
; Sequence 21, Application US/09573080A
; Patent No. 6828097
; GENERAL INFORMATION:
; APPLICANT: JOAN, KNOLL
; APPLICANT: ROGAN, PETER
; TITLE OF INVENTION: SINGLE COPY GENOMIC HYBRIDIZATION PROBES AND METHOD OF GENERATION
; FILE REFERENCE: 30307
; CURRENT APPLICATION NUMBER: US/09/573,080A
; CURRENT FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 479
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 21
; LENGTH: 8523
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: repeat_region
; LOCATION: (1)..(8523)
; OTHER INFORMATION: herv17
; PUBLICATION INFORMATION:
; PUBLICATION: Jurka, J; Malchiewicz, J; Milosavljevic, A
; TITLE: Prototypic sequences for human repetitive DNA
; JOURNAL: Journal of Molecular Evolution
; VOLUME: 35
; ISSUE: 4
; PAGES: 286-291
; DATE: 1992-10-
; DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
; DATABASE ENTRY DATE: 1996-01-26
; DATABASE ENTRY DATE: 1996-01-26

Query Match 80.8%; Score 6124.6; DB 4; Length 8523;
Best Local Similarity 95.7%; Pred. No. 0;
Matches 6363; Conservative 186; Mismatches 50; Indels 53; Gaps 27;

QY 606 GATGGAAACGTTCCCGCAAGACAAACCGCCCTAAGAGCTATTCTGGARAATTGGGA 665
DB 1923 GATGGAAACGTTCCCGCAAGACAAACCGCCCTAAGAGCTATTCTGGARAATTGGGA 1982

QY 666 MCAATTTGACCCCTCAGACACTAAGAAAGAAAGCACTTATTTCTGTCAGTCGCGCTG 725
DB 1983 CCAATTTGACCCCTCAGACACTAAGAAAGAAAGCACTTATTTCTGTCAGTCGCGCTG 2042

QY 726 GCATCTCTGGGGAAGTAAATATATACACCTTTACAGCTAGACVCTTTTGTAGAA 785
DB 2043 GCATCTCTGGGGAAGTAAATATATACACCTTTACAGCTAGACVCTTTTGTAGAA 2102

QY 786 AAGGCAATGAGTGAAGTGCCATTAAGTACAAACCTTTCTTTTCAATTAAGACAACTCAC 845
DB 2103 AAGGCAATGAGTGAAGTGCCATTAAGTACAAACCTTTCTTTTCAATTAAGACAACTCAC 2162

QY 846 AATTATGTAAAGTGTGATTTATGCCCTCAGGAAGCCTTCAGAGTCTACCTCCCTATC 905
DB 2163 AATTATGTAAAGTGTGATTTATGCCCTCAGGAAGCCTTCAGAGTCTACCTCCCTATC 2222

QY 906 CCAGCATCCCGACTCCTTCCCAATTAAGAGACCCCTTCAACCCAAATGGTCAA 965
DB 2223 CCAGCATCCCGACTCCTTCCCAATTAAGAGACCCCTTCAACCCAAATGGTCAA 2282

QY 966 AAGGAGATAGACAAAAGGGTAAACAGTGAAACAAAGAGTGCCAAATATTTCCCAATATGA 1025
DB 2283 AAGGAGATAGACAAAAGGGTAAACAGTGAAACAAAGAGTGCCAAATATTTCCCAATATGA 2342

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QY 1086 TCTCCAGACTTAAAGCAAAATATAAAGAGAGCTTAAATTTCTCAGATAATCTGATGG 1145
DB 2402 TCTCCAGACTTAAAGCAAAATATAAAGAGAGCTTAAATTTCTCAGATAATCTGATGG 2461

QY 1146 CTATATTGRTGTTTTTACAAGGGTTAGGACAAATTTCTTGATCTGACATGGAGAGATATA 1205
DB 2462 CTATATTGATGTTTTTACAAGGGTTAGGACAAATTTCTTGATCTGACATGGAGAGATATA-A 2520

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DB 2521 TGTCACTGCTAAATCAGACACTAAACCCCAATAGAGAGAGTGCCACCAATATCTGAGCCT 2580

QY 1266 GAGGTTTTGGCGATCTCTGTTATCTCAGTCAGTCAATGGATANGGATGACCAACAGAGG 1325
DB 2581 GAGGTTTTGGCGATCTCTGTTATCTCAGTCAGTCAATGG--ATAGGATGACCAACAG-AGG 2637

QY 1326 AAAGANAATGATTTCCCAAGCCAGCAGCTTCCAGTCTASACCTCATTTGGGGAC 1385
DB 2638 AAAGAGAAATGATTTCCCAAGCCAGCAGCTTCCAGTCTAGACCTCATTTGGG--- 2694

QY 1386 ACAGAAATCAGTAACATGGAGAGATTTGTTGTCAGACATTTGCTAACTTTGTTGCTASAA 1445
DB 2695 ACAGAAATCAGTAACAT--GGAGATTTGTTGTCAGACATTTGCTAACTTTGTTGCTAGAA 2753

QY 1446 GGACTAAGAGAAACTAGAGAAATCTAGCAATTTACTCAATGATGTCACCAATCAACACA 1505
DB 2754 GGACTAAGAGAAACTAGAGAG--AAGTCTATGAAATTTACTCAATGATGTCACCAATCAACACA 2812

QY 1506 GGGGAAGGAGAAATCTCTACTGCTTTCTGGAGAGACTAAGGAGGAGCATTTGAGGAAGC 1565
DB 2813 -GGGAGGAGAAATCTCTACTGCTTTCTGGAGAGACTAAGGAGGAGCATTTGAGGAAGC 2871

QY 1566 GTGCTCTCTGTCACCTGACTCTTCTGAAGGCCAACTAACTTTAAAGCGTAAAGTTTATCA 1625
DB 2872 GTGCTCTCTGTCACCTGACTCTTCTGAAGGCCAACTAACTTTAAAGCGTAAAGTTTATCA 2931

QY 1626 CTCACTCAGCTGCAGACATTTAG-AAAAAATTTCAAAAGTCTGCGGTAGGCGCCGAGGAGAA 1684
DB 2932 CTCACTCAGCTGCAGACATTTAGAAAAAATTTCAAAAGTCTGCGGTAGGCGCCGAGGAGAA 2991

QY 1685 ACTTAGAAACCTTATTGAACCTTGGCAACCTTGGTTTTTTTATATAGAGATCAGGAGGAGC 1744
DB 2992 ACTTAGAAACCTTATTGAACCTTGGCAACCTTGGTTTTTTTATATAGAGATCAGGAGGAGC 3051

QY 1745 AGCGGAAACAGGACAAACGGGATTTAAAAAAGGCCACCGCTTTAGTCATGACCTCTCAGG 1804
DB 3052 AGCGGAAACAGGACAAACGGGATTTAAAAAAGGCCACCGCTTTAGTCATGACCTCTCAGG 3111

QY 1805 CAAGTGAACCTTTGGAGGCTCTGGAAAGGAGAAAGCTGGGCAATTTGATCCCTTAATAGG 1864
DB 3112 CAAGTGAACCTTTGGAGGCTCTGGAAAGGAGAAAGCTGGGCAATTTGATCCCTTAATAGG 3171

QY 1865 GCTTGTCTCCAGTCGCGTCTACAGGACACTTTAAAAAAGATTTGTCAGGTAGAGTAAG 1924
DB 3172 GCTTGTCTCCAGTCGCGTCTACAGGACACTTTAAAAAAGATTTGTCAGGTAGAGTAAG 3231

QY 1925 CCGCCCTCTCGTCCATGCCCTTATTTCAAGGGAATCACTGGAAAGGCCCACTGCCCCAGG 1984
DB 3232 CCGCCCTCTCGTCCATGCCCTTATTTCAAGGGAATCACTGGAAAGGCCCACTGCCCCAGG 3291

QY 1985 GGCAGAAAGTCTTTTGTGATCAGAGCCACTAAACAGATGATCCAGCAGCAGGACTGAGGG 2044
DB 3292 GGCAGAAAGTCTCTGATGTCAGAGCCACTAAACAGATGATCCAGCAGCAGGACTGAGGG 3351

QY 2045 TGCTGGGGCAAGCGCCATCCCATGCCATCACCTCTCAGAGGCCCTGGGTATGCTTGACC 2104

QY 4265 GGAAAGRAAGGAAATAGAAAGGAAATGCAAGCAATATTTGAAGCAAAAGAGCTGCA 4324
DB 5533 GGAAAGGAAAGGAAATAGAAAGAACTGCAAGCAAGATATTTGAAGCAAAAGAGCTGCA 5592
QY 4325 AGGCAAGGACCTCCATTTAGAAATGCTATTAACCTTCCCTTAGTATAGGGTAAATCCCTTC 4384
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QY 4385 CGGGAACCAAGCCCACTAGCAAGGAGAAACAGAAATGGGAAACCTCAGAGG-CAG 4443
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QY 4504 CCAATGGGAATTTACTTTAAACCTTCAATCAAACTTTTCACTTAGGATCGATAGCACCA 4563
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QY 4564 TCARATGGCAATCAATTTACTTGGACCGGCTTTTCAAACTTTTCACTTAGGATCGATAGCACCA 4623
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QY 6424 GGCTCTTTCAGAACTATGCTCTCTCTTCTTAGTGCCCCCYATGRCCACTCTACACT 6483


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QY 4981 TGAAGGCCACAGTCCCTCAGGGAAGTTCGAGAAATGAATGAAYACTCAAGGACATCTA 5040
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Db 16671 AGAATCAAAACTCCCCCAAAAGCAGGACTTAGCCCATACGAAATGCTGTATGACAG 16612
QY 5161 CCCTTCATACCAATGACCTTGCTTGACCCA- AGACAGCCCAACTTAGTTGCAGACATC 5219
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QY 5220 ACCTCCTTAGCCAAATATCAACAAGTTCTTTAAACATTTACAGGAACCTATCCCTGAGAA 5279
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QY 5280 GAGGGAAGAACTATTCCACCWGTGACATGGTATTAGTCAAGTCCCTTCCTCTAAT 5339
Db 16491 GAGGGAAGGA- - -ATTCCACCTTGTTAAACATGGTATTAGTCAAGTCCCTTCCTCTAAG 16435
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Db 16374 GCAAGTTAAAGTGTCTGGAGTGGAGTCTTAGACACA- - -TCAAACCTGGATA 16326
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Db 16265 GATCTGACCTGCTCTTCAAGCAGACACTCGGAGGAAGTAACTGGAATCGTAGAGTCC 16206
QY 5580 CATGSGCTCCCTTATCATATTTTCTCTKTASTGTSTTTTAA- CCCTSTTTCACTCTCA 5638
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Db 16087 GAATGCGGCTTCCAGAAATATTGATGCCCATCGTATAGAGTCTTTTAAAGGGAACCC 16028
QY 5759 CCACTTCACTGCCACACCCATATGCCCCGCAACTGC 5796
Db 16027 CCACTTCACTGCCACACCCATATGCCCCGCAACTGC 5796
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RESULT 4
US-09-949-016-12249/c
; Sequence 12249, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

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; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
; FILE REFERENCE: CL001307  
; CURRENT APPLICATION NUMBER: US/09/949,016  
; CURRENT FILING DATE: 2000-04-14  
; PRIOR APPLICATION NUMBER: 60/241,755  
; PRIOR FILING DATE: 2000-10-20  
; PRIOR APPLICATION NUMBER: 60/237,768  
; PRIOR FILING DATE: 2000-10-03  
; PRIOR APPLICATION NUMBER: 60/231,498  
; PRIOR FILING DATE: 2000-09-08  
; NUMBER OF SEQ ID NOS: 207012  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 12249  
; LENGTH: 77997  
; TYPE: DNA  
; ORGANISM: Human  
; FEATURE:  
; NAME/KEY: misc_feature  
; LOCATION: (1)...(77997)  
; OTHER INFORMATION: n = A,T,C or G  
US-09-949-016-12249
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Query Match 39.5%; Score 2994.2; DB 4; Length 77997;  
Best Local Similarity 85.5%; Pred. No. 0;  
Matches 3418; Conservative 149; Mismatches 362; Indels 69; Gaps 23;  
  
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Db 19935 ACTTTGGAGGCTCTGGAAAGGGAAGCTGGGCAAAATCAAATGCCCTAGGCTTGCT 19876  
  
QY 1872 TCCAGTCCGCTACAGAGACACTTTAAAAAGATGTTCCNAGTAGAGTAAGCCGCC 1931  
Db 19875 TCCAGTGTGCTCTACAAGGACACTTTAAAAAGATGTTCTGAATAGAAATPAGCTGCC 19816  
  
QY 1932 TTGCTCATGCCCTTTATTTCAAGGGAATCACTGGAAGGCCCACTGCCAGGGGACAAA 1991  
Db 19815 -TATCCATGCCCTCATGTCAAGGGAATCACTGGAAGGCCCACTGCCAGGGGATGAA 19757  
  
QY 1992 GGTCTTTTGGTCCAGAACCCACTAACCCAGATGATCCAGCAGCAGGAGTGAAGGTGCTGG 2051  
Db 19756 GGTCTTTTGGTCCAGAACCCACTAACCCAGATGATGAGCAGCAGGAGTGAAGGTGCTGG 19697  
  
QY 2052 GGCAGGCGCATCCCATGCCATCACTCCCTCACAGAGCCCTGGGTATGCTTGACCATTGAGG 2111  
Db 19696 GGCAGGCGCATCCCATGCCATCACTCCCTCACAGAGCCCTGGGTATGCTTGACCATTGAGG 19654  
  
QY 2112 GCCAGGAAGGT- - -TGCTCTCTGGACACTGGTGGGTCTTCTTAGTCTTACTCTTCTGTC 2168  
Db 19653 GCCAGGAAGGTAACTGTCTCTGAACTGGCATGGCTTCTCAGTCTTAGTCTTCTGTC 19594  
  
QY 2169 CCGGACAACTGTCTCTCCAGATCTGTCACTATTCTGAGGGGCTCCNTAAGACGGGCACTCA 2228  
Db 19593 CTGGACAAACGCTCTCCAGATCTGTCACTACCC- - -GAGGGGCTCTAGGATAGGCACTCA 19537  
  
QY 2229 CTAGATACCTTTTTCAGGCCCACTAAGTTATGAACTGGGAGCTTTATTCTTTTCACTATGC 2288  
Db 19536 CTAGATAC- -TTCCTCCAGGCCCACTAAGTTATG- -ACTGGGGAACCTTCACTTTTCACTATGC 19479  
  
QY 2289 TTTTCTAATTTATGCTTTGAAGCCCACTACTCTTTTAGGGAGAGACATTTCTAGCAAAAGC 2348  
Db 19478 CTTTCTAATTTATGCTTTGAAGCCCACTACTCTTTTAGGGAGATACATTTCTAGCAAAAGC 19419  
  
QY 2349 AGGGGCCATTTATACACTTGAACTAGGAGAAAGCAACCCGTTTGTGTGTTGTTGTTGTTG 2408  
Db 19418 AGGGGCCATTTATACACTTGAACTAGGAGAAAGCAACCCGTTTGTGTTGTTGTTGTTGTTG 19361  
  
QY 2409 AGGAAGAAATTAATCTGAAGTCTGGGCAACAGAGAGCAATATGACGAGGCCAAAGAAAT 2468  
Db 19360 AGGAAGAAATTAATCTGAAGTCTGGGCAACAGAGAGCAATATATGATGAG- -GGAAGAAT 19302  
  
QY 2469 GCCCGTCTCTCAAGTAAACTTAAAGGATTCACCTTCCCTTCCCTACCAAGGACGATAC 2528  
Db 19301 GCCCGTCTCTCAAGTAAACTTAAAGGATTCGCGCTCTCTTCCCAACCAAGGACGATAC 19242
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QY	2529	CCCCTCAGACCCAAAGGCCCAACAAGGATTCCAAAAGATTGTTAAGGACTTTAAAGCCCAA	2588
Db	19241		19188
QY	2589	GGCTTAGTAAACCATGCATTAACCTCCCTGCAGTAATTCCTGTAGTGGATTGAGGAGGCACA	2648
Db	19181	GGCCCTAGTAAACCATGCATTAACCTCCCTGCAGTAATTCCTGTAGTGGATTGAGGAGGCACA	19129
QY	2649	GA AACCCAGTCGACAGTGGAGGGTTAGTGCAGATCTCAGGATTTCAATGGAGGCCGTT	2708
Db	19128	GA AACCCAAATGGACAGTGGAGGGTTAGTGCAGATCTCAGGATTTCAATGGAGGCCGTT	19071
QY	2709	GTCCCTTTTATACCCAGCTGTACCTAGCCCT---TATACTGTGMVTTCCCAATATACCAGAG	2765
Db	19070	GTTCCTCTATACCCAGCTGTACCTAATCTTATACTCACTCTGCTTTCCCAATATACCAGAG	19011
QY	2766	GAAGCAGAGTGGTTTACASTCCTCGACCTTMAAGSAGTCCCTTCTCTGCATCCCTGTACAT	2825
Db	19010	GAAGCAGAGTGGTTTACAGTCTCTGCACCTTAAAGSAGTCCCTTCTCTGCATCCCTGTACAT	18951
QY	2826	CCTGACTCTCAATTCCTTGTGTGCTTTGAAGATCTTCAACACCCARCATCTCAATCAGCC	2885
Db	18950	CCTGACTCTCAATTCCTTGTGTGCTTTGAAGATCTTGTGAATCTAATGTCTCAACACACC	18891
QY	2886	TGGACTRTTTTACCCCAAGGGTTTCAGGGATAGTCCCATCTAATTTGSCCAGSAGCTTAGCC	2945
Db	18890	TGGACTRTTTTACCCCAAGGGTTTCAGGGATAGTCCCATCTAATTTGSCCAGSAGCTTAGCC	18831
QY	2946	CAAGACTTGAGYCAATYMTCATCTCTGGACACCTCTGTCTCCTCRGTAKGTGGATGATTTA	3005
Db	18830	CGAGACTTGAGCCAGTTTCTCATACTTGGGCACCTCTGTCTCCTCRGTAKGTGGATGATTTA	18771
QY	3006	CTTTTRGCGCCYRFTTCAGAAACCTTGTGCCATCAAGCCACCAAGCRCCTCTTMAATTTC	3065
Db	18770	CTTTTRGCGCCACCAATTCAGAAACCTTGTGCCATCAAGCCACCAAGCRCCTCTTMAACTTC	18711
QY	3066	CTCGYACCTGTGTGCTACAMGGTTTCCAAACSAARARGCTCARCTCTGTCTCAGCAGCAGTT	3125
Db	18710	ATGSCCACCCTGTGGCTACAAGTTTTCAGACCAAGGCTCAGCTCTGCTCACAAGCAGTT	18651
QY	3126	AAATACTTTAGRCCTAARATTTATCCAAAGGCACAARGGCCCTCAGTGAGGAAYRYATCCAG	3185
Db	18650	AAATACTTTAGGGCTTAAATTTATCCAGACACACCAAGGCCCTCAGTGAGGAATGTCATCCAG	18591
QY	3186	CCATATCTGGCTTATCCTCATCTCYCAAACCTTAAAGCAACTAAGRBRPTCCCTGGCCTA	3245
Db	18590	CCATATCTGGCTTATCCTTATCCCAAAACCATTAAGCAATTAAGAGGGTTCCTTGGCATA	18531
QY	3246	AYAGGYTCTTCGCCGAATGGAATTCGCCAGGTTCGCCRAAATAGCCAGGYCAATTAAATAC	3305
Db	18530	ACAGGCTTCTGCCGATATGGATT---CCAGGTACAGTGAATATAGCCAGGCCAATTAATAC	18472
QY	3306	ASTAATTAAGGAATACTCAGAAAGCCCAATACCCATTTTARTAAGATGGAYAMCTGGAAYMRA	3365
Db	18471	ACTAATTAAGGAATACTCAGAAAGTGAATACCCATTTAGTAAAGGAAGCACCTTGAAGCAGA	18412
QY	3366	AGTGGCTTTCCAGGCCCTTAAAGAGCCCTTAAACCCAGYCCCAGTGTTAAGYTTGGCA	3425
Db	18411	AGTGGCTTTCCAGGCCCTTAAAGAGGCCCT---AATCCAGGCCCTAGTGTTAAGCTTTGCCA	18354
QY	3426	ACRGGGCAAGACTTTTSTTTATATYRTCACAGAAAAAACAAGAAVAGCTCTRGGAGTCCCT	3485
Db	18353	AAGGGCAAGACTTTTCTTATGTGTTCAG---AAAAACAAGGAATAGCTCTAGGATTCCT	18295
QY	3486	TACACAGRTCCRAGGAGYAGCTTGCAACCYRTGGCRVYACCTGASTAAAGGAAAYTGATGT	3545
Db	18294	TACACAGGTCRAGGAGACAGGTTGCAACCCATGGCATACCTGTAGTAAGGAAACTGATGT	18235
QY	3546	AGTGGCAAAAGGGTGTGCYTCATTTGTTTAVGGTAGTGTGGCAGTAGCAGTYKTAGTATC	3605
Db	18234	AGTGGCAAAAGGGTGTGCCTCATTTGTTTATGGGTAAATGGCAGCAGTAGCAGTCTTAGTATC	18175

QY	3606	TGAGCAGTTAAATAATACAGGGRAGAGATCTTACTGTGTGGACATCTCTCATGAKGTGAA	3665
DB	18174	TGAAGCAGTTAAATATCATACAGGGAAGAGATCTTACTGTGTGGATGTCTCATGATGTGGA	18115
	3666	YRGCACTACTCAGTCTAAAGGAGACTTGTGGCTGCAGACAAACVGTTTACTTTAAATRTCA	3725
DB	18114	CGGCATCTCACTGTCTAAAGGAGACTTACGGCTGTGCAGACAAACCGTTTGTCTTAAATATCA	18055
	3726	GGCTCTATTACTTTGAARGGCCAGTGTGCTGRACGTGTGCACCTTGTGCAACTCTTTAAACCCAGY	3785
DB	18054	GGCTCTATTACTTTGAARGGCCAGTGTGCGACTCGGCACCTGTGTCAACTCTTATATCCAGC	17995
	3786	CNCATTTCTTCAGACAATGAAGAAAGATARAAYATAACTGTCAACAARTAAATTTCTCA	3845
DB	17994	CACATTTCTTCAGACAATGAAGAAAGATATAAACAATAACTGTCAACAGGTGATTGCTCA	17935
	3846	AACTATGCCACTCGAGGGGACCTTGTAGARGTTCCYTTGACATGATCCYGACCTTCAACT	3905
DB	17934	AACTACGCCGTTCGAGGGGACCTCTAGAGGTTTCTTGTGACTGATCCCGACCTCAACT	17876
	3906	TGTATCTGATGGAAAGTTCTCTTTGTAGAAAAAGGACTTCCAAAAGYGGGGTATCGAGTGG	3965
DB	17875	TGTATCTGACGGAGTTCTCTTTGTAGAAAAAGCACTTCCAAAAGCAAGGTTATCGAGTGG	17816
	3966	TCAGTGATAATGGAATAYTTGAAAGTAATCCCTCTCACTCCAGGAACCTAGTCTYAGCTRG	4025
DB	17815	TCAGTGATAATGGAATACTTTGAAAGTAATCCCTCTCACTCCAGGAACCTAGCGCTCAGCTGG	17756
	4026	CAGAACTAATAGCCVTCATYKGGGCACCTAGAAATTTAGGAGAAAGBAAAAGGGYAAATATAT	4085
DB	17755	CAGAACTAATAGCCCTCACTCAGGCACTAAATTTAGGAGAAAGBAAAAGGGTAAATATAT	17696
	4086	ATACAGACTCTRTATATGCTYACCTAGTCTCCTCATGCCATGMRGCAATATGTSARAGAAA	4145
DB	17695	ACACAGACTCTAAGAAATGCTTACTTAGTCTCTCATGCCCCATGCGACAAATATGGAGAAA	17636
	4146	GGGAATTCCTAACTTCYAGRGAAACACCTATCAMACATCAGGAAGCCATTAGGARATTAT	4205
DB	17635	GGGAATTCCTAACTTCGAGGGAAACACCTATCAAACTCTCAGGAAGCCATTAGGAGATTAC	17576
	4206	TATYGGGCHGTACAGAAACCTATAGAGGTGGMAGTCTTACACTCYGGGGTCATCANAAG	4265
DB	17575	AATTGGCTGTACAGAAACCTTAAAGAGGTGGCAGTCTTACACTCCCGGGGTGATCAGAAAG	17516
	4266	GAAAGRAAAGGGAATAAAGGAAATGTCACAGCAKATATTGAAGCMAAAGAGCTGCAA	4325
DB	17515	GAAAGRAAAGGGAATAAGAGGAACCGCGAAGCAGATCTGAAGCCAAAAGAGCCGCAA	17456
	4326	GGCAGGACCCCTCCATTAGAAATGCTTATTAACCTTCCCTTAGTATAGGGTAATCCCTTCC	4385
DB	17455	GGTGGGACCCCTCCATTAGAAATGCTTATAGAGGACCCCTAGTATGGGGTAATCCCTGT	17396
	4386	GGGAACCAAGCCCCAGTACTCAGCAGGGAACAGAAATGGGGAACTCACAGGGCAGTT	4445
DB	17395	AGGAACCAAGCCCCAGTACTCAAAAGAAATAGGATGGGGAACTCACAGGAGCATAGTT	17336
	4446	TTCTCCCTCGGGAACGGTTTAGCCACTGAAGAAGGGGAAAATACCTTTTTCCTGCAACTATCC	4505
DB	17335	TCTTCCCTCAGGATGGCTAGCCACCGAAGAAAGGAAAATACCTTTTTCCTGCAAGTAAAC	17276
	4506	AATGGAAATTAATCTTAAAAACCTTTCATCAAAACCTTTTTCACCTTAGGCATCGATAGCACCATC	4565
DB	17275	AATTGAAATTAATCTTAAAAACCTTTCATCAGACCTTTTTCACCTTAGGCATCGATAGCACCATC	17216
	4566	ABATGGCCAAATCATATTTTACTTGACACAGGCTTTTTCAAAACCTATCAAGACBATAKTCA	4625
DB	17215	AGACGGCCAAATCATATTTAATCTGATCAGGACTTTTTCAAAACCTATCAAGACAGATAGTCA	17156
	4626	GGGCTGTGAATGTGGCCABARAATAATCCCTGCCTVATCCCAAGCTCCTTCAGGAR	4685
DB	17155	GGGCTATGAAGTGTGGCAAGAAATAATCCCTGCCTTATCCCAAGCTCCTTCAGGAR	17096
	4686	AACAAARAAACAGGCCATTACCTCTGRARAARACTGGCAACT-GAATTTTACCACAAGCCCCA	4744

Db 17095 AACAAAGAAAGGCGCAATACCCAGGAGAGACTGGCAACTAGATTTTACCCACATGCCCCA 17036
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Db 17035 AATCTCAGGATTTTCAGTATCTACTAGCTCGGGTATATATCTTTCAGGGTTGGGCARAGG 16976
Qy CTTTCCCTCTAGGACAGAAAGGCCCAAGAGGTAATAAAGGCACTAGTTTCATGAATAA 4864
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Qy TTCCAGATTCGAGATTTCCCGAGGCTTACAGAGTGAATAAGCCCTGCTTTTCAGGCCA 4924
Db 16915 TTCCAGATTCGAGATTTCCCGAGGCTTACAGAGTGAATAAGCCCTGCTTTTCAGGCCA 16856
Qy CAGTACCCAGGAGTATCCAGGCG---TTAGGTATAGATATCACTTACACTGGCC 4980
Db 16855 CAGTACCCAGGAGTATCCAGGCGTTACTTAGGCATACAATATCACTTACACTGGCC 16796
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Db 16795 TGAAGGCCACAGTCTCTCAGGAAAGGTCGAGAAATGAATGAAATCAAGAGACATCTA 16736
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Qy GATTTGGCTGCTCTTCAACACAAACACAGGAGAAAGTAACTAAATCATATAATCCCC 5579
Db 16269 GATCTGCACTGCTCTTCAAGGACAACTCGAGGAAAGTAACTGGAATCTGTAGCTCC 16210
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Db 16209 --ATGGCCCCCCCCGTCATATTTTCTTCTTACGTGTGCTTACCCCCCTTCACTATCA 16152
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Db 16091 GAATGCGGCTTCCCAAGAAATATGATGCCCCCATCTATAGAGTCTTTTSTAAGGAAACCC 16032
Qy CCACCTTCACTGCCCCACACCCCATATGCCCCGCACTGC 5796

Db 16031 CCACTTTCCATCCACACCCCATATGCCCTGCACCTTC 15994
RESULT 5
US-09-175-928-3
; Sequence 3, Application US/09175928A
; Patent No. 6312921
; GENERAL INFORMATION:
; APPLICANT: Jacobs, Kenneth
; APPLICANT: McCoy, John M.
; APPLICANT: LaVallie, Edward R.
; APPLICANT: Collins-Racie, Lisa A.
; APPLICANT: Evans, Cheryl
; APPLICANT: Merberg, David
; APPLICANT: Treacy, Maurice
; APPLICANT: Mi, Sha
; APPLICANT: Genetics Institute, Inc.
; FILE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
; TITLE REFERENCE: 6006B.Au172A
; CURRENT APPLICATION NUMBER: US/09/175,928A
; CURRENT FILING DATE: 1998-10-20
; NUMBER OF SEQ ID NOS: 62
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 2946
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-175-928-3
Query Match 38.1%; Score 2888.6; DB 3; Length 2946;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 2872; Conservative 49; Mismatches 3; Indels 1; Gaps 1;
Qy 4658 CTCCTVATCGCCAAAGCTCTCTCAGGARAACAARAACAGGCCATTACCTGRRARAC 4717
Db 6 CTCCTTATCGCCAAAGCTCTCTCAGGARAACAARAACAGGCCATTACCTGGAAGAC 65
Qy 4718 TGGCAACTGATTTTACCACAAGCCCAACCTCAGGGATTTTCACTAGTCTGGG 4777
Db 66 TGGCAACTGATTTTACCACAAGCCCAACCTCAGGGATTTTCACTAGTCTGGG 125
Qy 4778 TATATCTTTCAGGGTTGGGCARAGGCTTCCCTCTAGGACAGAAAGGCCCAAGAGG 4837
Db 126 TAGATATCTTTCAGGGTTGGGCARAGGCTTCCCTCTAGGACAGAAAGGCCCAAGAGG 185
Qy 4838 TAATAAAGGCACATAGTTTCATGAATAATTCACAGATTCGGACTTCCCGAGGCTTACAGA 4897
Db 186 TAATAAAGGCACATAGTTTCATGAATAATTCACAGATTCGGACTTCCCGAGGCTTACAGA 245
Qy 4898 GTGCAATAGCCCTGCTTTCCAGGCCACAGTAACCCAGGGAGTATCCAGGCGTTAGGTA 4957
Db 246 GTGCAATAGCCCTGCTTTCCAGGCCACAGTAACCCAGGGAGTATCCAGGCGTTAGGTA 305
Qy 4958 TACGATATCTTACATCTGCGCTTGAAGGCCACAGTCTCTAGGGAAGTTCGAGAAATGA 5017
Db 306 TACGATATCTTACATCTGCGCTTGAAGGCCACAGTCTCTAGGGAAGTTCGAGAAATGA 365
Qy 5018 ATGAAAYACTCAAGAGCATCTTAAAGCAAAACCCAGGAACCCACCTCACATGGCCTG 5077
Db 366 ATGAAAYACTCAAGAGCATCTTAAAGCAAAACCCAGGAACCCACCTCACATGGCCTG 425
Qy 5078 YTCGTTGCTTATAGCTTAAAAAGAAATCTGCAACTTTTCCCAAAAAAGCAGGACTTAGCC 5137
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Qy 5198 AGCCAACTTAGTTCGAGACATCCTCTCTAGCCAAATATCAACAAGTCTTTTAAACATT 5257
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Db 2765 AGAATAGCCCAATCATCTATTGCTGAGAGCACAGCAGGAGGACAATGATCGGATATA 2824
Qy 7478 AACCCAGTATTCAGCGCGCAACCGCAACCCCTTTGGGTCCCTCCCTTTGATGGGA 7537
Db 2825 AACCCAGTATTCAGCGCGCAACCGCAACCCCTTTGGGTCCCTCCCTTTGATGGGA 2884
Qy 7538 GCTCTGTTTTCATGCTATTTTCATCTCTATTAAATCTTGCARCTGCR 7582
Db 2885 GCTCTGTTTTCATGCTATTTTCATCTCTATTAAATCTTGCARCTGCA 2929

RESULT 6
US-09-949-016-13002/c
; Sequence 13002, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13002
; LENGTH: 168394
; TYPE: DNA
; ORGANISM: Human
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)..(168394)
; OTHER INFORMATION: n = A,T,C or G
US-09-949-016-13002

Query Match 34.5%; Score 2615.4; DB 4; Length 168394;
Best Local Similarity 85.1%; Pred. No. 0;
Matches 3133; Conservative 134; Mismatches 355; Indels 58; Gaps 33;

Qy 1012 TTCCCCCAATATGACCCCTCCCAAGCAGTGGGAGGAGAGATTCGGCCCAAGCCAGAGTG 1071
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Qy 1072 CATGTGCTTTTCTCCAGACTTAAAGCAAAATAAAACAGACTTAGGTAAATTTCTCA 1131
Db 28945 TATGTACCTTTTCCCTGTGAGACTTGAAGCAAAATAAAATAGACCTTAGGTAAATTTCTCA 28886
Qy 1132 GATAAATCTGATGCTATTTGTTTGAAGGTTTGAACAATTTCTTTGATCTGACA 1191
Db 28885 GATAAATCTGTTGGCTATTTGATGCTTTTCAAGGGTTAGACAATCTTTGATCTGACA 28826
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Qy 1252 CATAACTCAGCCTGAGGTTTGGGATCTCTGGTATCTCAGTCAAGTCAATGGATANGG 1311
Db 28766 CATAACTCAGCCTGAGAGTTTGGGATCTCTGGTATCTCAGTCAAGTCAATG--ATAGG 28709
Qy 1312 ATGACAAAGAGGAAAGANAATGATTCGCCACAGGCCAGCAGCAGTTCACGTTTASA 1371
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Qy 1432 CTGTGTGCTASAGGACTAAGGAAATCTASGAAAGAAATCTATYGAATTTCAATGATG 1491
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Qy 1612 GCCTAAATTTATCATCTCAGTCAGCTGAGACATTTAG-AAAAAATCTCAAAGTCTGCCGT 1670
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Db 28358 AGGCCAGAGCAAACTTTAGAAACCTTATTTGAATCTTGGCAACTTCGGTTTTTATATATAG 28299
Qy 1731 AGATCAGGAGGAGCAGCGGGAACAGGACAAACGGGATTTAAAAAAGGCCCAACCGCTTTAG 1790
Db 28298 AGATCAGGAGGAGCAGCGGGAACAGGATAAACGGGA-TAAAGAAAAGGCCCAACTTTAG 28240
Qy 1791 TCATGACCCCTCAGCAGAG-TGGACTTTTGGAGGCTCTGGAAGGGAAGAGCTGGGCAAT 1849
Db 28239 TCATGGCCCTCAGCAGACGACTTCGAGGGCTCTGGAACAGGAAAGTCTGGACAAT 28180
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Qy 2029 GCAGCAGACTGAGGTCCTGGGCAAGCGCCATCCCATGCCATCACTCCCTCACAGAGCC 2088
Db 27999 GCAGCAGACTGAGGTCCTGGGCAAGCGCCATCCCATGCCATCACTCCCTCACAGAGCC 27940
Qy 2089 CTGGGTATGCTTGACCACTTGAAGGCCAGGAAGGT---TGTCTCTGGAACACTGGTGGCGT 2145
Db 27939 CCGGTATGCTTAACCACTTGAAGGCCAGGAAGTTAACTGTCTCTGGACACTGGCGTGGC 27880
Qy 2146 CTTCTTATGCTTACTCTTCTGTCGGGCAAACTGTCTCTCAGATCTGTCACTATTTCTGAG 2205
Db 27879 CTTCTCAGTCTTACTCTCTGTCCTGGAACACTGT-CTCCAGATCTGTCACTATCCAAAG 27821
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Qy 2266 GGAGCTTTATTTTTCATGCTTTTCTAATATGCTTTGAAAGCCCACTACCTTTGTTA 2325
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Qy 2386 CCGTTTGTGTCCTGCTTGGAGGAGGATTAATCTCAGAGTCTGGGCAAGAGG 2445
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Qy 2446 ACAATATGAGCAGCAAAAGATGCCCTCTCTGTTTCAAGTTTAAATTAAGGATTTCCACTT 2505
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Qy	2626	CCGTAGTGGATTGAGGAGGACAGAAACCCAGTGGACAGTGGAGGGTTAGTGCAGAGATCT	2685
Db	27411	C-----AATTTTAGGAGTAAAGAAGCCCAATAGACAGTGGAG--GGTTAGTACAAAGATG	27360
Qy	2686	CAGGATTATCAATGGAGGGCGTTGTCCTTTTATACCCAGCTGTACCTAGCCCTTATACTG	2745
Db	27359	CAGGATTATCAGT-GAGGCTGCTGTTCTCTATACCCAGCTGTACCTTACCCCTTCTACTC	27301
Qy	2746	TGMYTTCCCAAAATACAGAGGAAAGCAGAGTGGTTTACASTCTCTGGACTTTMAGGATGCCT	2805
Db	27300	TGCTTTCCCAAAATACCAGAGGAAGCAGAGTGGTTTACAGTCTCGACCTTAAGGATGCCT	27241
Qy	2806	TCCTCTGCAATCCCTGTACATCTCGACTCTCAATTCCTGTTGCTTTGCTTTGAAGATCTTCAA	2865
Db	27240	TTTCTGCAATCCCTGTACATCTCGATTCCTCAATTCCTTATTTGGCTTTTAAAGATGCTTCAA	27181
Qy	2866	ACCCARCACTCTCAACTCACCTGGACTTTTACCCCAAGGGTTTCAGGAGTAGTCCCATC	2925
Db	27180	ACCCAATGCTCAACTCACCTGGACTGTTTACCCCAAGGGTTAAGATAGGCCACATC	27121
Qy	2926	TATTTGGCCAGGCATTTAGCCCAAGACTTGAGYCARITYMTCATCTACCTGGACACTTTGTCC	2985
Db	27120	TATTTGGCCAGGCATTTAGCTCAAGACTTGAGACAGTTCTCATACCTGACAGCTTTGTCC	27061
Qy	2986	TTTCRTAGTGAATGATTTACTTTTTRGCGCCVRRTT-CAGAAACCTTGTGCCATCAAGCC	3044
Db	27060	TTTGTTGATCATGGATTAATCTACTTCTAGCTGCCTGTTTGAIAAAACCTTGTGCCATCAAGCC	27001
Qy	3045	ACCCAAGRCCTCTTMAATTTCTTCGCVACTGTGGCTACAGGTTTCCCAACCSARAGCT	3104
Db	27000	ACCCAAGCGCTTTTAACTTCTCTCACCTTTGGCTTCAAGGTTTCCCAACCAAGGCT	26941
Qy	3105	CARCTCTGCTCACAGCAGTTAAATACTTAGGCTAARATTTATCCAAAGGCACACAGGCC	3164
Db	26940	CAGCTCTGCTTACAGCAGTTAAATACTTTAGGCTTAAATTTCCAAAGGCACACAGGCC	26881
Qy	3165	CTCAGTGAAGAAAYRATCCAGGCTTATCTGGCTTATCTCTCATCYCAAAACCTTAAAGCAA	3224
Db	26880	CTCAGTAAAGAAATGTATCCAGGCTTATCTGGCTTATCTCTCATCCCAAAACCTTAAAGCAA	26821
Qy	3225	CTAAGRGRTTCTTTGGGRTAAVAGGYTCTCGCGAAWTGGATTCCTCAGGTTGGCRA	3284
Db	26820	ATAAAG-GTTTCTTTGGCATACAGGCTTCTGCGAAATATGGATT-CCCAGGTACGGCAA	26763
Qy	3285	AATAGCCAGGYCATTTAWATACASTAATTAAGGAAACTCAGAAAGCCAAATACCCATTTATT	3344
Db	26762	AATAGCCAGGCATTTATATACACTAATTAAGGAACTCAGAAAGCCAAATACCCATTTAGT	26703
Qy	3345	AAGATGGAYMCTGAAGYWRAGTGGCTTTTCAGGCCCTTAAAGAGGCTTAAACCCAA	3404
Db	26702	AAAAATGGACTCTCCTAAGCAAAAGCAGCTTTCAGGCCCTTAAIAAAAGGCGCTT-AAAGCAA	26644
Qy	3405	GYCCAGTGTTAAGYTTGCGCAACRGCGCAAGACTTTTSTTYATRYTCAAGAAAAAAC	3464
Db	26643	GACTCAGTGTTAAGCTTACCAACGGGGCAAGACTTTTCTTCATATGTCAC--AAAAAAC	26587
Qy	3465	AGRAAYAGCTCTRGAGTCTTTACAGRTCCRAGGGYAGGCTTGCACACCVRTGGCRA	3524
Db	26586	AGAAATAGCTCCAGGAGCTTTACAGGTTCAAGGGACCGAGCTTGCAACCATGGCAT	26527
Qy	3525	CCTGASTAAGGAAAYTGATGTAGTGGCAAGGGTTGRCVYTCATGTTTAYGGGTAGTGT	3584
Db	26526	CCTAAGTAAGAAAAATTAATGTAGTGGCAAGGGTTGGCATCATTTGTTTACGGGTAGTGGC	26467
Qy	3585	GGCAGTAGCAGTYKTAGTACTGAAGCAGTTAAAAATAATACAGGGGAGAGATCTTACTGT	3644
Db	26466	GGCAGTAGCAGCTTGTAGTATGTAAGCAGTTTAAAAATAATACAGGGAAGAGATCTTACTGT	26407

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RESULT 7
US-09-949-016-15858/c
; Sequence 15858, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 15858
; LENGTH: 145320
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-15858

Query Match          29.3%; Score 2220.4; DB 4; Length 145320;
Best Local Similarity 86.6%; Pred. No. 0;
Matches 2728; Conservative 92; Mismatches 216; Indels 115; Gaps 32;

QY 606 GATGGGAAACGTTCCCGCAGACAAACAAACGCCCCCTAAGACGTATTCGGAATTTGGGA 665
DB 97137 GATAGGAAACGTTCCCTCAAGGCAAAACACCCCTAAGATGTATTCGAGAAATTTGGGA 97078

QY 666 MCAATTTGACCCCTCAGACACTAGAGAGAAACGACTTATATCTCTCGAGTGCCTG 725
DB 97077 CCAATTTGACTCTCAGATGCTAAGAAAAAAGAAC--ATATTTCTTCGACGTACCGCTG 97020

QY 726 GCA-----CTCCTGAGGGAAGTATAAATATAA 753
DB 97019 GCAACGATATACTTTTAAGGGGAGAAACCTGCGATCCTGAGGGAAGCATAAATATAA 96960

QY 754 CACATCTTACAGCTAGACACTTTTGTAGAA---AAGGCAAAATGGAGTGAAGTGCATA 810
DB 96959 CACCATCTTACAGCTAGACCTCTTTGTAGAAAAGAGGCAAAATGCTGTGAAGTGTGATA 96900

QY 811 AGTACAACTTTCTTTTCAATTAAGACAACTCAATATATGTAAAAGTGTGATTTATG 870
DB 96899 CGTACAAACTTTCTTTTCAATTAAGACAACTCGCAATATATGTAAAAGTGTGATTTATG 96840

QY 871 CCCTACAGGAAGCCTTCAGAGTCTACCTCCCTATCCAGCATCCCC--GACTCCTTCCCC 928
DB 96839 CCCTACAGGAAGCCTTCAGAGTCTACCTCCCTATCCAGCATCCCCAGACTCCTTCCCC 96780

QY 929 AMYTAATAAGGACCCCCCTTCAACCCAAATGGTCCAAAAGAGATAGACAAAAGGGTAAA 988
DB 96779 AAATAATAAGGACCCCCCTTCAACCCAAAACGGTCCAAAAGAGATAGACAAAAGGGTAAA 96720

QY 989 CAGTGAACCAAGAGTGCATATATCCCAATATATGACCCCTCCCAAGCAGTGGGAGAA 1048
DB 96719 CAACTAACCAAGAAATGCCAATATATCCCGCATATATGCCCCCTCC--AAGCGGTGGAG 96664

QY 1049 GAGAAATTCGGCCAGCAGAGTGCATGTGCTTTTCTCCAGACTTAAAGCAAAATAA 1108
DB 96663 GAGAAATTCGGCCAGCAGAGTGCATGTGCTTTTCTCTCTCAGACTT----TAAATTA 96608

QY 1109 AAACAGACTTAGGTAATTTCTCAGATAAYCTGTAGTGTATATTTGRTTTTTTCAAGGGT 1168
DB 96607 AAATAGACCTTAGGTAATTTCTCAGATAACCCCTAATGGCTATATTTGATGTTTTTCAAGGGT 96548

QY 1169 TAGACAACTTTTGTATCTGACATGGAGAGATATATATGTCACCTGCTTAATCAGACACTA 1228
DB 96547 TAGACAACTTTTGTATCTGATATGGAGAGATATA-ATGTTACTGCTTAATCAGACACTA 96489
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QY 2303 TTGAAGGCCCACTACCTCTGTAGGAGAGACATCTACCAAAAGCAGGGCCATTATAC 2362
DB 95423 CTGAAGGCCCACTCCCTCTGTAGGAGAGACATCTAGCAAAAGCAGGGCCATTATAC 95364
QY 2363 ACCTGAACATAGGAGAGAAACACCGTTTGTGTCCTCTCTGAGGAAGGAATTAAT 2422
DB 95363 ACCTGAACATAGGA-----GAACACCGTTTGTGT-CCCTCTCTGAGGAAGGAATTAAT 95309
QY 2423 CTTGAAGTCTGGGCAACAGAGGACAAATATGGACGAGCCAAAGAAATGCCCTCTCTGTCA 2482
DB 95308 CTTGAAGTCTGGGCAACAGAGGACAAATATGGACGAG-CAAGAAATGCCCTCTGTCA 95250
QY 2483 AGTTAAACTAAAGGATTCACATTCCTTCCCTACAAAGGAGTACCCCTCAGACCCAA 2542
DB 95249 AGTTAAACTAAAGGATTCCTCTCTCTTCCCAAAAGGAGTACCCCTTAGACCCGA 95190
QY 2543 GSCCAACAGAGATTCCTAAAGATTTGTAAGGACTTAAAGGCCCAAGGCTAGTAAACC 2602
DB 95189 GSCCTCAACAGGACTCCAAAGA-----TTAAGGACCTTAAAGGCCCAAGGCTAGTAAAGC 95133
QY 2603 ATGCATAACTCCCTGCAGTAATTCCTGTAGTGAATGAGGAGGCACAGAAACCCAGTGGAC 2662
DB 95132 ATGCATAAGCCCTACATAATCC-----NACTTAGGAGTACAGAAACCCAGTGGAC 95080
QY 2663 AGTGAGGGTTAGTCAAGATCTCAGGATATCAATGAGGAGCGGTGCTTTTATACCC 2722
DB 95079 AGTGGA-GGTTAGTCAAGATCTCAGGATATCAAT-GAGGTCACTGCTCCCTCTATACCT 95022
QY 2723 AGCTGTACTAGCCCTTACTGTGMYTCCCAATACAGAGGAGCAGAGTGTATTAC 2782
DB 95021 AGCTGTACTAGCCCTTATCTCTCTTCCCAATACAGAGGAGCAGAGTGTATTAC 94962
QY 2783 ASTCTGACCTTMAAGTAGCTTCTCTGATCCCTGTACATCTGACTCTCAATCTT 2842
DB 94961 AGACTGTAGCTTAAGTAGCTTCTCTGATCCCTGTACATCTGACTCTCAATCTT 94902
QY 2843 GTTGGCTTTGAAGTATCTTCAAAACCCARCTCACTCACTGAGATTTTACCCCA 2902
DB 94901 ATTTGGCTTTGAAGTATCTTCAAAACCCARCTCACTCACTGAGATTTTACCCCA 94842
QY 2903 AGGTTTCAGGATAGYCCCATCTATTGGCCAGGCATTTAGCCCAAGCTTGGACARTY 2962
DB 94841 AGGTTTCAGGATAGYCCCATCTATTGGCCAGGCATTTAGCCCAAGCTTGGACCGTT 94782
QY 2963 MTCATACCTGTGACACTCTGTCTCTGTAAGTGGATGA--TTTACTTTTTCGTCCTCT 3020
DB 94781 CTCATACCTGGGACTCTGTCTCTGTAAGTGGATGA--TTTACTTTTTCGTCCTCT 94722
QY 3021 TCAGAAACCTTGTGCAATCAAGCCACCCAGCTCTTMAATTTCTCGYACCTGTGGC 3080
DB 94721 TCAGAAACCTTGTGCAATCAAGCTCAACCAAGTCTCTTAAATTTCTCGCTACCTGTGC 94662
QY 3081 TACAWGTTTCCAAACARAGCTCARTCTGCTCAGAGGTTTAAATCTTAGGRTA 3140
DB 94661 TACAWGTTTCCAAACCAAGGCTCAGCTCTGCTCAGAGGTTTAAATCTTAGGRTA 94602
QY 3141 ARATTATCCAAAGGACCAAGGCCCTCAGTGGAGAAVYATCCAGCTTACTGCTTAT 3200
DB 94601 ARAATTATCCAAAGGACCAAGGCCCTCAGT-----GCCATTCTGCTTAT 94556
QY 3201 CCTCATCYCAAAACCTTAAAGCAACTAAGRRRTTCTTTGGORTAAYAGGTTTCTGCCGA 3260
DB 94555 CCTCATCYCAAAACCTTAAAGCAACTAAGAGGTTTCTTTGATATACAGGTTTCTGCCAA 94496
QY 3261 AWATGGATTCCTCAGGTTGGRAAATAGCCAGGTCATTATATACASTAATTAAGGAAC 3320
DB 94495 ATATGGATT-CCCAGGTTACGGGAATATAGCCAGACCATTTATATACASTAATTAAGGAAC 94437
QY 3321 TCAGAAAGCCCAATACCCATTTTARTAAGATGGAYAMCTGAAGYMRAGTGGCTTTCCAGGC 3380
DB 94436 TCAGAAAGCCCAATACCCATTTTARTAAGATGGAYAMCTGAAGYMRAGTGGCTTTCCAGGC 94377
QY 3381 CCCTAAAGAGGCCCTTAAACCCAGYCCAGTGTAAAGYTTTGCCAAACRGGGCAAGCTTT 3440

RESULT 8

US-09-949-016-5640
; Sequence 5640, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5640
; LENGTH: 2763
; TYPE: DNA
; ORGANISM: Human
US-09-949-016-5640

Query Match 29.1%; Score 2204; DB 4; Length 2763;
Best Local Similarity 98.4%; Pred. No. 0;
Matches 2194; Conservative 35; Mismatches 0; Indels 1; Gaps 1;

QY 5352 GATACATCTCTGGGAGGACCTACCCAGTCACTTTTATYACCCCACTGCGGTAAAGTG 5411
DB 535 GATACATCTCTGGGAGGACCTACCCAGTCACTTTTATCTACCCCACTGCGGTAAAGTG 594
QY 5412 GCTGAGTGGAGTCTTGATACATCACCTTGAGTCAATCTTGATCTGCAAGGAA 5471
DB 595 GCTGAGTGGAGTCTTGATACATCACCTTGAGTCAATCTTGATCTGCAAGGAA 654
QY 5472 CCTCAAAATCCAGAGACCAACGCTAGCTATTCTGTGAACCTCTAGAGGATTTGCGCTG 5531
DB 655 CCTCAAAATCCAGAGACCAACGCTAGCTATTCTGTGAACCTCTAGAGGATTTGCGCTG 714
QY 5532 CTCTTCAAAACCAACAGGAGGAAAGTAATAAATCAATAATCCCATGSGCTCC 5591
DB 715 CTCTTCAAAACCAACAGGAGGAAAGTAATAAATCAATAAT-CCCATGSGCTCC 773
QY 5592 TTATCATATTTTCTCTKTASTGTTSTTTTACCCTSTTTTCACTCTCACTGCAACCCCTCC 5651
DB 774 TTATCATATTTTCTCTTACTGTTCTTTTACCTCTTTTCACTCTCACTGCAACCCCTCC 833


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: SEQ ID NO 26
: LENGTH: 8399
: TYPE: DNA
: ORGANISM: Homo sapiens
: FEATURE:
: NAME/KEY: repeat region
: LOCATION: (1)..(839)
: OTHER INFORMATION: henv9
: PUBLICATION INFORMATION:
: AUTHORS: Jurka, J; Malchiewicz, J; Milosavljevic, A
: TITLE: Prototypic sequences for human repetitive DNA
: JOURNAL: Journal of Molecular Evolution
: VOLUME: 35
: ISSUE: 4
: PAGES: 286-291
: DATE: 1992-10-
: DATABASE ACCESSION NUMBER: Database of repetitive elements (repbase)
: DATABASE ENTRY DATE: 1996-01-26
: DATABASE ENTRY DATE: 1996-01-26
US-09-573-080A-26

Query Match      28.6%; Score 2168; DB 4; Length 8399;
Best Local Similarity 67.6%; Pred. No. 0;
Matches 3334; Conservative 143; Mismatches 1354; Indels 103; Gaps 34;

Qy      605 TGATGGGAAACGTTCCCGCAAGACAAAAACGCCCTTAAGACGTATTCTGGARAATTGGG 664
Db      1276 TGATAGGAACACTCAGGCATCAACCGCTCACCTTGAATGTATCTTAAGCCATTGGG 1335

Qy      665 AMCAATTGACCTTCAGACACTAAGAAAGAAACGACTTATATCTTCTGCAGTCCCGCCT 724
Db      1336 ACCAATTGACCAACAAACCTGAAAGAGGCGACTCATTTTCTGCACACTACGCT 1395

Qy      725 GGCAC-----CCTGACGGGAAGTATAAATTATA 752
Db      1396 GACCTTAATATCTCTCTGTGATGGGGAAAAATGCCACCTTGAGGGGAAGTATAAATTACA 1455

Qy      753 ACACCATCTTACAGCTAGACVCTCTTTGT---AGAAAAGGCAATGAGATGAAGTGCAT 809
Db      1456 ATACTATCTGCAGTTGACCTTTCTGTAGAGGGAGGTAAATGAGTGAATATACAT 1515

Qy      810 AAG----TACAACTTTCTTTTCATTAAGAGACAACTCACAATTTATGTAAGAGTGTGAT 865
Db      1516 AAGGTATTACAAGCTTCTTTTCTTCACTGAAGGAGAATACAACTATGCAAGCTTGCAT 1575

Qy      866 TTATGCCCTACAGAAAGCCTTCAGAGTCTACCTCCCTATCCAGCATCCCGACTCCCTTC 925
Db      1576 TTACATCCCAAGGAGGACCTTTTCAGTCTACCCCATATCCTAGCTCCCTAGAGCTCTC 1635

Qy      926 C--CCAMYTAAATAGGACCCCTCTTCAACCCAAATGTGTCAAAAGGAGATAGACAAAGG 983
Db      1636 CTTCCTATTATGCAAGCTCTCTCCATCTCCCTGCCAAGAGGAAATAAGCAAGAA 1695

Qy      984 GTAACAGTGAACCAAGAGTGCCAAATATCCCAATATGACCCCTCCCAAGCAGTGGG 1043
Db      1696 ATCTCAAGAGGACCAAAAAACCTCGGCTATCGGTTATGTCCCTT-CAAGCTGTAGG 1754

Qy      1044 AGGAAGAGAAATTCGGCCAGCAGAGTGCAATGTGCYTTTIVYTCGCCAGACTTAAGACA 1103
Db      1755 GGGTGGAGAAATTTGGCCCAACCCAGGTACATGTCCCTTCTCCCTCTGTGATTTAAAGCA 1814

Qy      1104 AATAAAACAGACTTAGTAAATCTCAGATAA'CCCTGATGGCTATATTGTGTTTTTACA 1163
Db      1815 GATCAAGGCAGACTGGGGGAAGTTTTCAGATGAT'CTCTGATAGGCACATAGATGTCCTCCA 1874

Qy      1164 AGGGTTTAGGCAATTTCTTGTATCTGATGGAGAGATATATGTCACTGCTAAATCAGA 1223
Db      1875 GGGTCTAGGCAACCTTCGATCTCACTTGGAGAGATGT-CATGCTATTGTTAGATCAA 1933

Qy      1224 CACTAACCCCAATAGAGAGAGTGCCACCAATACTGACGCTGAGTGTTTGGGATCTCT 1283
Db      1934 CCTGGCTTTAATGAAGAAATGTCGCTGTAGCTGCAGCTGAGAGTTTGGAGATACCT 1993

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Db 5189 CTTAAAAACCTCCACAAACCTTTTCATATGGGTATTTGAAAAACATCATCAATGGCCACA 5248
Qy 4577 TCATTATTTACTGACAGGCTTTTCAAACTATCAAGCARATATKTCAGGCGCTGTGAA 4636
Db 5249 TCTCTATTCAGAGCCCAATCTACTCTGGGCTTCCACAGGTAGTCAAACTGTGAG 5308
Qy 4637 KTGTGCCARAAAAATATCCCTCCTCTATCGCCAAAGCTCTTCCAGGARAACAARAACA 4696
Db 5309 GTGTGCCAAAGGAATAATCCCTGGTCCATGTGAAGGCCATTTTGGGGGAACAAGAATA 5368
Qy 4697 GGCATTTACCTGPARAARACTGCAACTGATTTTACCACAA--GCCAAACCTCAGGG 4754
Db 5369 GGTCACTATCTGAGAGGACTGCGAGTACAGCTTACCCCATATGGCTAAATCAAAAGG 5428
Qy 4755 ATTTCAGTATCTACTAGTCTGGGTARATATCTTTCACGGTGTGGCARAGGCTTCCCTCG 4814
Db 5429 ATTTCATATCTTGTGTCTGTGTATACCTTTACAATTTGGATAGAGCTTCCCTCG 5488
Qy 4815 TAGACAGAAAGCCCAAGAGGTAATAAAGGCACTAGTTTCATGAATAATTTCCAGATT 4874
Db 5489 CAAGACAGAGAAGACTCAGGAAGTGAATTGAAGTCTTAATGATGAATAATTTCTAGATT 5548
Qy 4875 CGGACTTCCCGAGGCTTACAGATGACAATAGCCCTGCTTTCAGGCGCAGTAACCCA 4934
Db 5549 TGGGCTTCCCTAAGGCTTACAGAGTGAATGGTCCAG-TTTTAAAGCCCAATAACTCA 5607
Qy 4935 GCGAGTATCCAGGCTTGTAGTATACGATATCACTTACACTGCGCTTGAAGGCCACAGTC 4994
Db 5608 GGGANTGTCAGGCTGTGGGATACAGTATCACTTTCATCTGCGCCCGAGGCCCAATC 5667
Qy 4995 CTGAGGAAGGTCCGAAAAATGAATGAAYAYACTCAAAAGGACATCTAAAAAAGCAAAACCCA 5054
Db 5668 CTGAGGAAGGTCAAGAAGGCAAAATGAAGAACTCGAGGCACTTAAGGAACCTAACACAAG 5727
Qy 5055 GGAACCCACCTCATCTGGCTGTCTGTGGCTATAGCTTAAAGAAATCTGCAACTT 5114
Db 5728 GAA-----CATCTCCATGGCTACTCTTTTGGCCATGGCTTGTGAGAATCCGAAATTC 5783
Qy 5115 TCCCCAAAAGAGGACTTAGCCATACGAATGCTGTATGGAGGCGCTTCAACCAA 5174
Db 5784 TCCTCAAAAATGGGCTCAGTCCATATGAATGCTGTATGGACAAATTTTCTCAAAA 5843
Qy 5175 TGACCTTGTCTGTACCCCAAGACAG-CCAAATTTAGTTGCAGACATCACTCTTTAGCCAA 5233
Db 5844 TGACCTCTTCTGTATGAGGAAGAAAGAACTTGTTCAAAGATATACTTCTTCGCAAA 5903
Qy 5234 ATATCAACAAGTCTTAAACAATTACAAAGAACTTATCCCTGAGAGAGGAAAGAACT 5293
Db 5904 ATATCAACAACAAACCTTAAACAACTTACCTGAAGGATGTACAGAGAAAGGAAACAGAGTT 5963
Qy 5294 ATTCCACCCWGTGACATGTATTAGTCAAGTCCCTCTCTCTAAATTTCCCATCCCTAGA 5353
Db 5964 GTTTCACACAGGAGATCTAGTGTGGTCAAAATCTCTCCCTCTACCTTCCCTCATCTATGGA 6023
Qy 5354 TACATCTCTGGAAGGAGCCCTTACCCAGTCAATTTATYACCCCACTCGGCTTAAAGTGGC 5413
Db 6024 CTCTCTGTGGGAAGGCTACTACTCAATAATCTCTTACCCACACTGCACTGAGTGGT 6083
Qy 5414 TGAGTGGAGTCTTGGATACATACACTTGGATCAAAATCTCGATATCTGCAAGGAACC 5473
Db 6084 AGGAGTGAATCTTGGATTCCACACACCCGAGTTAAATTTTGGACATCTCCCTGAGGAACC 6143
Qy 5474 TGAATATCCAGGAG 5487
Db 6144 TGTGAGACCATCAG 6157

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RESULT 10

US-08-979-847B-87

; Sequence 87, Application US/08979847B

; Patent No. 6582703

; GENERAL INFORMATION:

; APPLICANT: PERRON, HERVE

```

;
; BESEME, FREDERIC
; BEDIN, FREDERIC
; PARANHOS-BACCALA, GLAUCIA
; KOMURIAN-PRADEL, FLORENCE
; JOLIVET-REYNAUD, COLETTE
; MANDRAND, BERNARD
; GARSON, JEREMY
; TUKE, PHILIP
;
; TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
; ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPH
; THERAPEUTIC PURPOSES
;
; NUMBER OF SEQUENCES: 210
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OLIFF & BERRIDGE, PLC
; STREET: P. O. BOX 19928
; CITY: ALEXANDRIA
; STATE: VA
; COUNTRY: USA
; ZIP: 22320
;
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PC-DOS/MS-DOS
; APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US/08/979.847B
; FILING DATE: 26-No. 6582703-1997
; CLASSIFICATION: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: BERRIDGE, WILLIAM P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPB 39046A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 703-836-6400
; TELEFAX: 703-836-2787
;
; INFORMATION FOR SEQ ID NO: 87:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2304 base pairs
; TYPE: nucleotide
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 87:
;
; US-08-979-847B-87
;
; Query Match 24.2%; Score 1837.4; DB 4; Length 2304;
; Best Local Similarity 87.2%; Pred. No. 0;
; Matches 2032; Conservative 119; Mismatches 150; Indels 29; Gaps 15;
;
; Qy 2025 TCCAGCAGCAGGAGCTGAGGCTGCTGGGGCAAGCGCATCCCATGCCATCACCTCACAG 2084
; Db 1 TCCAGCAGCAGGAGCTGAGGCTGCTGGGGCAAGTGCAGGCCATGCCATCACCT--CAG 58
; Qy 2085 AGCCCTGGGTATCTTACCATTTGAGGCGCAGGAAGGT---TGTCTCTGGACACTGGTG 2141
; Db 59 AGCCCGGGTATCTTTCACCATTTGAGAGCCAGGAAGTAACTTCTCTCGACACTGGCG 118
; Qy 2142 CGGTCTTCTTAGTCTTACTCTTCTGTCGCGGCAACTGTCTCCAGATCTGTCACTATTC 2201
; Db 119 CAGCCTTCTCAGCTTACTTCTCTGTCGCCAGAAATTTGCTCCAGATCTGTCACTATTC 178
; Qy 2202 TGAGGGGGTCCNTAAGACGGGCGAGTCACTAGATACCTTTTTCGCCAGCCACTAAGTTATGAA 2261
; Db 179 ---GAGGGGTCTTAGACAGCGCAGTCACTACATAC--TTCTCTCAGCCACTAAGTTGTG-A 233
; Qy 2262 CTGGGAGCTTTATTTCTTTTCACTGCTTTTCTAAATATGCTTTGAAAGCCCACTACTT 2321
; Db 234 CTGGGAACTTTACTCTTTTCACTGCTTTTCTAAATATGCTTTGAAAGCCCACTACTT 293
; Qy 2322 GTTAGGGAGAGACATTTCTAGCAAAAGCAGGGCCATTATACCTGAAACATAGGAGAGG 2381
; Db 294 GTTAGGGAGAGACATTTCTAGCAAAAGCAGGGCCATTATACCTGAAACATAGGAGAGG 353
; Qy 2382 AACACCCGTTTGTGTGTCNCCCTGCTTTGAGGAAGGAATTAATCTCTGAAGTCTGGGCAACAG 2441

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Db 354 AATACCAATTGCTGT-CCCTGCTTGGAGGAATTAATCCTGAAGTCGGCAATAG 412
Qy 2442 AAGGACAAATATGACAGCCAAAGAAATGCGCTGCTGTTCAAGTTAACTTAAGGATTC 2501
Db 413 AAGGACAAATATGACAG-CAAAGAAATGCGCTGCTGTTCAAGTTAACTTAAGGATTC 471
Qy 2502 ACTTCTCTTTCCCTTACCAAGGAGTACCCCTCAGACCCAAAGGCCCAACAAGGATTC 2561
Db 472 GCTCTCTTTCCCTTACCAAGGAGTACCCCTTAGACCCGAGGCCCTCAAGGAGTCA 531
Qy 2562 AAGATGTTAAGGACTTAAAGCCAAAGGCTTAGTAAACCAATGCAATACTCCCTGAGT 2621
Db 532 AAGATGTTAAGGACTTAAAGGCCAAAGGCTTAGTAAACCAATGCAATACTCCCTGCAAT 591
Qy 2622 AATTCGTTAGTGGATTGAGGAGCAGAAACCCAGTGGACAGTGGAGGTTAGTGCAG 2681
Db 592 ACTCC-----AATTTTAGGAGTAAGGAAACCCAGGACAGTGGAG-GGTTAGTGCAG 643
Qy 2682 ATCTCAGGATTAATCAATGAGGCGGTTGCTCTTTTATACCAGCTGTACTAGCCCTTAT 2741
Db 644 ATCTCAGGATTAAT-AGGCTGTTTTTCTCTATACCAGCTGTACTAGCCCTTAT 702
Qy 2742 ACTGTGMYTTCCCAATACCAGAGGAGCAGAGTGGTTTACASTCTCGGACCTTMAAGGAT 2801
Db 703 ACTCTGCTTTCCCTAATACCAGAGGAGCAGAGTGGTTTACAGTCTCGGACCTTAAAGGAT 762
Qy 2802 GCCTTCTTGCACTCCCTGATACATCTGACTCTCAATTCTGTTGCTTGAAGTACT 2861
Db 763 GCCTTTTCTGCACTCCCTGATCTGCTGACTCTCAATTCTGTTGCTTGAAGTACT 822
Qy 2862 TCAACCCCAACACTCAACTGACTCTTTTACCCCAAGGTTTCAGGGATAGYCCC 2921
Db 823 TTGAACCAACGCTCACTCACTGACTGCTTTTACCCCAAGGTTTCAGGGATAGCCCC 882
Qy 2922 CATCTATTTGGCCAGGCAATTAGCCCAAGACTTGAGTCAAATTCCTCATACCTGGACACTCT 942
Db 883 CATCTATTTGGCCAGGCAATTAGCCCAAGACTTGAGTCAAATTCCTCATACCTGGACACTCT 942
Qy 2982 GTCCCTTCRGTAKGTGATGATTTACTTTTTRGCTGCGYRTTCAGAAACCTTGTGCCATCA 3041
Db 943 GTCCCTTCAGTACGTGGATGATTTACTTTTAGTCGCGCGTTTCAGAAACCTTGTGCCATCA 1002
Qy 3042 GCCACCAACGCTCTTMAATTTTCTCGYACCTGTGGCTACAGGTTTCCAAACASARAR 3101
Db 1003 GCCACCAACGCTCTTMAATTTTCTCGYACCTGTGGCTACAGGTTTCCAAACCAAG 1062
Qy 3102 GCTCARCTCTGCTCACAGCAGGTTAAATACTTAGGCTTAARATTTATCCAAAGGCCAC 3161
Db 1063 GCTCGGCTCTGCTCACAGGAGATTAGATCTTAGGCTTAAATTTATCCAAAGGCCAC 1122
Qy 3162 CCTCAGTGAAGAYATCCAGCTTATCTGCTTATCTGCTATCTATCTATCTATCTATCT 3221
Db 1123 GCCTCAGTGAAGAACCTATCCAGCTTATCTGCTTATCTGCTTATCTATCTATCTATCT 1182
Qy 3222 CAATAGGRRRTTCTTGGCTAAAGYTTCTGCGGAATGATTTCCCAAGTGTGG 3281
Db 1183 CAATAGGRRRTTCTTGGCTAAAGYTTCTGCGGAATGATTTCCCAAGTGTGG 3281
Qy 3282 CHAATAGCCAGGCTTATWATACASTAATTAAGGAACTCAGAAAGCCCAATACCCATTT 3341
Db 1242 CCCAATAGCCAGGCTTATWATACASTAATTAAGGAACTCAGAAAGCCCAATACCCATTT 1301
Qy 3342 ARTAAGATGGAYMCTCAAGTGAAGTGGCTTCCAGGCGCTTAAAGAGGCTTAAACC 3401
Db 1302 AGTAAGATGGACACT---ACAGAGTGGCTTCCAGGCGCTTAAAGAGGCGCTT---AACC 1356
Qy 3402 CAAGYCCAGTGTAAAGYTTGCCAACCGGCAAGCTTTTSTTATATVATACAGAAAAA 3461
Db 1415 CAAGCCCCAGTGTTCAGTGTGCCAACAGGCGAAGATTTTCTTATATGCCACAG-AAAA 1415
Qy 3521 AACAGAAATAGCTCTGAGGTCCTTACACAGTCCAGGAGYAGCTTGCACACCTTGGC 3521

Db 1416 AACAGAAATAGCTCTAGGAGTCTTTACGCAAGTCTCAGGATGAGCTTGCACACCCCTGGT 1475
Qy 3522 AACCTGASTAAGGAAATGATGTAGTGGCAAGGTTGRCYTCATTGTTTATYGGGTAGT 3581
Db 1476 ATACCTGAGTAAGGAAATGATGTAGTGGCAAGGTTGCGCTCATGTTTATGGGTAA 1535
Qy 3582 GGTGCAGTAGCAGTYKTATGATATGAAAGCAGTTAAATAAATACAGGAGAGATCTTAC 3641
Db 1536 GCGCAGTAGCAGTCTTAGTATCTGAAGCAGTTAAATAAATACAGGAGAGATCTTAC 1595
Qy 3642 TGTGTGCACTCTCATGAGTGAAYRGCACTCACTGCTTAAAGGAGATCTTGGGCTGTC 3701
Db 1596 TGTGTGCACTCTCATGAGTGAAYRGCACTCACTGCTTAAAGGAGATCTTGGGCTGTC 1555
Qy 3702 AGACAACATCTTAAATRTCAGGCTCTATTTACTTGAARGGCCAGTGTGCRACCTGTG 3761
Db 1656 AGACAACATCTTAAATRTCAGGCTCTATTTACTTGAARGGCCAGTGTGCRACCTGTG 1715
Qy 3762 CACTTGTGCACTCTTAAACCCAGYCNCACTTCTTCAGACAATGAAGAAAGATARAAYA 3821
Db 1716 CACTTGTGCACTCTTAAACCCAGYCNCACTTCTTCAGACAATGAAGAAAGATARAAYA 1775
Qy 3822 TAACTGTCAACAATTAATTTCTCAACCTATGCCACTCGAGGAGCTTCTTACAGTCTCC 3881
Db 1776 TAACTGTCAACAATTAATTTCTCAACCTATGCCACTCGAGGAGCTTCTTACAGTCTCC 1835
Qy 3882 YTTGACTGATCCVAGCTTCAACTTGTATATGATGGAAGTTCCTTTGTAGAAAAAGGAC 3941
Db 1836 CTTGACTGATCCGACC-TCACTTGTATATGATGGAAGTTCCTTTGGCAGAAAAAGGAC 1894
Qy 3942 TTGAAAAAGYGGGGTATGAGTGGTCAAGTGAATTAATGGAATATTTGAAAGTAATCCCTCA 4001
Db 1895 TTGAAAAAGYGGGGTATGAGTGGTCAAGTGAATTAATGGAATATTTGAAAGTAATCCCTCA 1954
Qy 4002 CTTCCAGGAATAGTGTAGCTGAGCAACTATGCCCTCACTCGAGGAGCTTCTTACAGTCT 4061
Db 1955 CTTCCAGGAATAGTGTAGCTGAGCAACTATGCCCTCACTCGAGGAGCTTCTTACAGTCT 2014
Qy 4062 GAGAGAAAAAGGGYAAATATATATACAGACTCTTAAATATGATGCTTACCTAGTCTTCCATG 4121
Db 2015 GAGAGAAAAAGGGYAAATATATATACAGACTCTTAAATATGATGCTTACCTAGTCTTCCATG 2074
Qy 4122 CCCATGRCGAATATGSAAGAAAGGAAATCTTAACTTCYAGAGCAACCTATATCAAC 4181
Db 2075 CCCATGRCGAATATGSAAGAAAGGAAATCTTAACTTCYAGAGCAACCTATATCAAC 2134
Qy 4182 ATCAGAGCCATTAGGATTAATTTATGCGCTACAGAACTTARAGAGTGGAGTCT 4241
Db 2135 ATCAGAGCCATTAGGATTAATTTATGCGCTACAGAACTTARAGAGTGGAGTCT 2194
Qy 4242 TACACTGCGGGCTCATANAAAGGAAAGGAAATASAAAGRAAYTGCCCAAGCAK 4301
Db 2195 TACACTGCGGGCTCATANAAAGGAAAGGAAATASAAAGRAAYTGCCCAAGCAK 2254
Qy 4302 ATATTGAAGCAAAAAAGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 4351
Db 2255 ATATTGAAGCAAAAAAGAGTGCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 2304

RESULT 11

US-09-949-016-13840

; Sequence 13840, Application US/09949016

; Patent No. 6812339

; GENERAL INFORMATION:

; APPLICANT: VENTER, J. Craig et al.

; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

; FILE REFERENCES: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

; CURRENT APPLICATION NUMBER: US/09/949,016

; CURRENT FILING DATE: 2000-04-14

; PRIOR APPLICATION NUMBER: 60/241,755

; PRIOR FILING DATE: 2000-10-20

; PRIOR APPLICATION NUMBER: 60/237,768

; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 13840
 ; LENGTH: 276687
 ; TYPE: DNA
 ; ORGANISM: Human
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (1)...(276687)
 ; OTHER INFORMATION: n = A,T,C or G
 ; US-09-949-016-13840

Query Match 19.9%; Score 1507.4; DB 4; Length 276687;
 Best Local Similarity 68.3%; Pred. No. 0;
 Matches 2289; Conservative 94; Mismatches 914; Indels 52; Gaps 24;

Qy	697	CGACTTATATCTCTCGCAGTCCCGCTGGCACTCTGAGGAAAGTATAAATTATAACAC	756
Db	27184	CCAATATTTCTCTCTGATGGGAAATAATGGCCACTCTGAGGAAGTACAAATTACATAC	27243
Qy	757	CATCTTACAGCTAGACATCTTTTGTAGAA--AAGCAAAATGGAGTGAAGTGCCTAAGT	813
Db	27244	TATCTGAGCTTGACCTTTTCTGTAAGAGGGAAGCAAAATGGAGTGAATACCTTATGT	27303
Qy	814	ACAAACTTTCTTTTCAATTAAGAGCAACTCAAAATATGTAAGAGTGTGATTATGCC	873
Db	27304	CCAAGCTTTCTTTTCAATTAAGAGCAACTCAAAATATGTAAGAGTGTGATTATGCC	27363
Qy	874	TACAGGAAGCTTTCAGAGTCTACCTTCCCTATCCAGCATCC--CGACTCTCTCCCCAM	930
Db	27364	CACAGGAGGACCTCTCAGCTCACCCCATATCTAGCTCCCTATAGCTCCCTTCTAT	27423
Qy	931	YTAATAAGAACCCCTTCAACCCAAATGGTCCAAAGAGATAGACAAAAGGGTAAACA	990
Db	27424	GAATGATAATCTCTCTAATCTCCCGCCGCGGCAAGAAATAAGCAAGAAATCTCCA	27483
Qy	991	GTGACCAAAAGAGTCCCAATATTTCCCAATATGACCCCTCCAGCAGTGGGAGGAAGA	1050
Db	27484	AAGGACCAAAACCTCTCTGCTATATGGTATGTCCCT--TCAAGCTGTAGGGGGAGGG	27542
Qy	1051	GAATTCGGCCAGCCAGAGTGCATGCTGCTTTTCTCCAGACTTAAAGCAATAAAA	1110
Db	27543	GAATTCGGCCAAACCGGGTACATGCTCCCTTCTCCCTCTCGAATTAAGCAGATCAAG	27602
Qy	1111	ACAGACTTAGGTAAATTTCTCAGATAATCTGATGGCTATATTTGTTTAAAGGGTTA	1170
Db	27603	GCAGACCTGGGAAGTTTTCAGATGATCTCTGATAGTACATAGATGTCTTACAGGTCTA	27662
Qy	1171	GGACAAATTTTGTATCTGACATGGAGAGATATATATGTCATCTGCTAAATCAGACATAAC	1230
Db	27663	GGGCAAACTTTCGACCTCGCTGGAGAGATGT--CATGCTACTGTGAGATCAAACTTGGC	27721
Qy	1231	CCCAATCAGAGAAGTGCACCATACCTGAGCTGAGGTTTGGCGATCTCTGCTATCT	1290
Db	27722	CTTAAATGTAAGAATGCGCTTTAGCTGACGCCAAGAGTTGGAGATACCTGCTATCT	27781
Qy	1291	CAGTCAGGTCAATGGATGAGTACAAACAGAAAGGAAGANAATGATTTCCCAAGGCCA	1350
Db	27782	TAGTCAAGTAAATG--ATAGAATGACAGCGGAAAGAGGACAAATTTCCCTACCGGTCA	27838
Qy	1351	GCARGCAGTCTCCAGTCTASACCTCATTTGGGACACAGAAATCAGTAACATGGAGATT	1410
Db	27839	GCAACCCATCCCAATATGGATCCCACTGGGACC--TTGACTTCAGATCATTGGGACT	27894
Qy	1411	GGTGTGACAGACATTTGCTTAACTTGTGCTASAGGACTAAGGAAACTAGAGGAAR	1470
Db	27895	GGATCATAAACATCTGTTGACCTGTATTTAGAAAGGACTAGGAGAATTA--GAAAAAG	27953
Qy	1471	TCTAYGAATTAATCTCAATGATGTCCACCATATAACACAGGGGAAGGAAATCTTACTGC	1530

Db	27954	CCCATGAATTAATCAATGATGTCCGCCATAACTCA--GGGAAAGGAAGAAATCTCTTCTGC	28012
Qy	1531	CTTTCTGAGAGACTAAGGGAGGCATTCAGGAAGGCTGCTCTCTGTACCTGACTCTTC	1590
Db	28013	CTTCTCGAGCGGTACGGGAGGCTTAAGAAATATATACTCCCTGTCAACCCGAATCACT	28072
Qy	1591	TGAAGGCCAACTAATCTTAAAGCGTAAGTTTATCACTCAGTCAGCTGAGACATTAAGAA	1650
Db	28073	TGAGGTCATTTGATCTTAAAGATAGTTTATTAACCCAGTCAGCCACAGATATCAGGAG	28132
Qy	1651	AAACTTCAAAAGTCTGCGTAGGCGGAGCAAACTTAGAAAACTTATTAACCTTGGCA	1710
Db	28133	AAAGCTCGAAAAGCAATCCAGGGCCCTGAAACAAATCTAGAGGCTATTTAAACCTGGCA	28192
Qy	1711	ACYTCGGTTTTTATATAGAGATCAGGAGGAGCGGACAGGACAAACGGGATTA	1770
Db	28193	ACCTCGGTGTTCTATAATAGGACCAAGAGAAACAGGCCCAAAAGGAAGGAGATCAG	28252
Qy	1771	AAAAAGGCCACCGCTTTAGTCATGACCTCAGGCAAGTGACTTTGGAGGCTCTGGAAA	1830
Db	28253	AGAA--AGGCCGAGCCTTAGTCATGGCCCTCAGACAAACAACTTGGTGGTTCAGAGAG	28311
Qy	1831	AGGAAAAGCTGGGCAATTCGATCCCTAATAGGCTTTGCTTCCAGTGGCTCAAGG	1890
Db	28312	GACAGAAAATGGAGCAGGCCAATCACCTGGTAGGGCTTGTATACAGTGTGTTACTAGG	28371
Qy	1891	ACACTTTAAAAAGATGTCCTCAAGTAGAAGTAAGCCGCCCTTCTGTCATGCCCTTATT	1950
Db	28372	ACACTTTAAAAAGATGTCCTCAATGAGAAAACAGGCTGCCCTCTGTCATGTCCTCATATG	28431
Qy	1951	TCAAGGGAATCACTTGAAGGCCCACTGCCCCAGGGGACAAAGGTCTTTTGTAGTCAGAAAG	2010
Db	28432	CCGAGGCAATCACTTGAAGGTGCACTGCCCCAGAGGACGAGATTCCTTGGTGGTCAAGG	28491
Qy	2011	CACATAACAGATGATCGAGCAGGAGCTAGGAGTGCCTGGGGCAAGGCCCATCCCATGC	2070
Db	28492	CCCCAACAGATGATCAACAAACAGGAGCTAGGGGTGCGCGGGCAAGGCCAGCTCATGT	28551
Qy	2071	CATCACCTCACAGAGCCCTGGGTATGCTTACCATTTAGGCCCAAGGAA--GGTTGTCT	2127
Db	28552	CATCACCTCTACTAGCCCGGGGTATGTTTAACTATTAGGGGCCAGGAAATGACTTCT	28611
Qy	2128	CCTGGAACACTGGTGGGTCTTCTTACTTCTTCTGTCGGGACAACTGTCTCTCCAG	2187
Db	28612	CCTGGAACACTGGGACGGCTTCTCAGTGTAACTCTCTGCTGGATGACTGTCTCAGG	28671
Qy	2188	ATCTGTCACTATCTGAGGGGTCCNTAAGACGGGAGTCACTAGATACTTTTCCCAGC	2247
Db	28672	----TCCCTTACCATCCGAGGAATCCTGGGACAGCTGTAAACCAGGTA--TTTCTCCACC	28726
Qy	2248	CACATAAGTTAAGTGGGAGCTTTTATCTTTTTCATGCTTTTCTTAATTTATGCTTGA	2307
Db	28727	TCCTCAGTTGT--AAATTGGAAGACTTTGCTCTTTTTCATGCTCTTTTGTGTGCTGAA	28785
Qy	2308	AGCCCCACTACTTTTGGGAGAGACATTCAGCAAAAGCAGGGCCATTTATACACCTG	2367
Db	28786	AGTCCCACTACTTTTGGGAGGATATATAGCAAGGTGGAGCTTTATCTACATG	28845
Qy	2368	AACATAGGAGAAACACCCGTTTGTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTGTTG	2427
Db	28846	AATATGAGAAACAAAGTTTACCCATTTTGTGT--CCCTTACTTGGAGGGGAAATCAACCTGA	28904
Qy	2428	AGTCTGGGCAACAGAGGACATATGACGAGCCAAAGAAATGCGCGTCTGTTCAAGTTA	2487
Db	28905	AGTCTGGGCAATGGAAGGACAAATTTGGAAG--GGCAAAAAATGCTGCGCCAGTCCAATCA	28963
Qy	2488	AACTTAAAGGATTCACCTTCTTCCCTACCAAGGAGTACCCCTCAGACCCCAAGGCC	2547
Db	28964	GGTTTAAAGATCCCACTTTTCTTATCAAAAGGCAATATCCCTTAAGGCTGAGGCTC	29023
Qy	2548	AACAGGATTCAAAAGATTTGTTAAGGACTTTAAAGCCCAAGGCTTAGTAAACCATGCA	2607
Db	29024	ATAAAGGATTACAGAAATATTGTTTAAACATTTGAAAGCTCAAGGCTTAGTGAGAAATGCA	29083

QY 2608 TAACCTCCCTGCAGTAATTCGGTAGTGAGTTCAGGAGGACAGAAACCCAGTGGAGCTGG 2667
Db 29084 GCAGTCCCTGCAACACACCC-----AATTCAGAGTACAAAACCTGAACGGTCAGTGG 29136
QY 2668 AGGTTAGTGCAGAGATCAGGATTAATCAATGGAGGCGGTGTCTTTTATATACCAGCTG 2727
Db 29137 A-GACTAGTGAAGATCTTAGACTCATCAAT-GAGGAGTAATTTCCACTATATCCAGTTG 29194
QY 2728 TACCTAGCCCTTATACGTGMYTTCCCAATATACCAGAGGAGCAGAGTGGTTTACASTCC 2787
Db 29195 TACCAACCCCTATACCCCTCTCTCAATATACCAGAGGAGCAGAGTGGTTTACAGGTTG 29254
QY 2788 TGGACCTTMAAGGATCCCTCTCTGTCATCCCTGTACATCTCTCAATCTTCTTGTGTTG 2847
Db 29255 TGGACCTCAAGGATCCCTCTCTCTGTTATCCCTGCACTCTGATTCOCAGTTCCTCTTTG 29314
QY 2848 CTTTGAAGATACCTTCAACCCARCATCTCACTCACTGACCTGACCTTTTACCCCAAGGTT 2907
Db 29315 CTTTGAAGATCCCAAGGATCCCAAGGATCCCAAGGATCCCAAGGATCCCAAGGTT 29374
QY 2908 TCAGGATAGYCCCACTCTATTTGGCCAGGATTCAGCCCAAGCTTCAGYCATYMTTCAT 2967
Db 29375 TTAGGATAGCCCTCATCGGTTTGGTCAGGCCCTAGCCCAAGATCTAGGCCACTCTCTCAA 29434
QY 2968 ACCTGGACACTCTTGTCTTCRGTAKGTGGATGATTTTCTTTTTCGCGCCYRITTCAGAAA 3027
Db 29435 GTCCAGGCACTCTGTCTCTTCAATATATGAGTATGATTTTGTGCTACCAAGTTCAGAA 29494
QY 3028 CTTTGTGCCATCAAGCCCAAGCCTCTTMAATTTCTCGCYVACCTGTGGCTTACAWGG 3087
Db 29495 CTTGTGCCAGCAGGCTACTAGACTCTTTGAATTTCTAGCTGATCAAGGGTACAAAGG 29554
QY 3088 TTTCCA-AACASARAGTCACTCTGTCTCAGCAGGATTAATACTTAGGCTTAARATTA 3146
Db 29555 TGCTAGGTGGAAGGCCAGCTTTTGCTACAGCAGGTTAAATATCTAGGCTTAATCTTA 29614
QY 3147 TCCAAAGCCACAGGCGCTCAGTGAGGAAYATCCAGCTATATCTAGGCTTATCTTCAT 3206
Db 29615 GCCAAGGGACAGGCGCTCATCAAGGAGGATACAGCTTACTGGCTTATCTTTCG 29674
QY 3207 CYCAAAACCTTAAAGCAACTAAGRGRTCTTGGCTTAAYAGYTTCTGCCGAATATGG 3266
Db 29675 CTTCAGACATTAACAAGTCTTGGGGTCTCTGGAATTAAGCTTGGCGGACTATGG 29734
QY 3267 ATTCCCGAGTTCGCAATAGCAGGCTATTAATATACATAATTAAGGAATCTCAGAA 3326
Db 29735 A-TCCCGGATACAGCGAGATAGCCAGGCCACTCTGTACGCTAATCAAGGACACCCAG 29793
QY 3327 AGCCAATACCCATTTARTAGATGGAYAMCTGAAGYRAAGTGGCTTTCCAGGCGCCCTAA 3386
Db 29794 GGCAATATAC-----TCTGTTGGATCAGAGCAGAAACAGCTTCAAACTTAA 29845
QY 187 AGAAGGCTTAAACCCAGYCCCAAGTGTAAAGYTTGCAACRGGGCAAGACTTTTSTTAA 3446
Db 29846 CGAGGCGCT--AGTACAAGCTCCAGCTTTAAGGCTTTCCCAAGTACAAAGCTTCTCTTA 29903
QY 3447 TAYTCAAGAAAAAAGCAAGAAAGCTCTGGAGTCTTACACAGRTCCBAGGAGYAG 3506
Db 29904 TACGTACAG-AGAGAGCGGGATAGCTCTTGGAGTCTTACTCAGACTCGTGGGACAA 29962
QY 3507 CTTGCAACYRTGGCRVACCTGASTAAGGAAATGATGTAGTGGCAAGGGTTCRCYTCA 3566
Db 29963 CCCACCAAGTGGCATACCTAAGTAAAGAAATGATGTAGTAAAGGCTGGCTCA 30022
QY 3567 TTGTTTAYGGTGTGTGGCAGTAGCTAGTATCTGAAGCAGTATAAATAATACA 3626
Db 30023 CTGTTTAAGTGTAGTTCAGCAGTGGCGCTCTTAGTGTACAGACTATCAAAATAATACA 30082
QY 3627 GGRAGAGATCTTACTGTGTGGACATCTCATGAKGTGAAYGCACTACTCAGTCTAAAG 3686
Db 30083 AGGAAAGGATCTCACTGTCTGACTACTCATGATGTAATGGCATACTAGGTGCCAAAG 30142

QY 3687 AGACTTGTGGCTCTCAGACAAACGTTTACTTAAATRTCAGGCTCTATTACTTGAARGCC 3746
Db 30143 AAGTTTATGCTATCAGACAGCCACCTACTTAGATACAGGTCCTCTCTTGAAGGACC 30202
QY 3747 AGTGCTGCRACCTGTCACCTGTGCAACTCTTAAACCCAGYCNCAATTTCTCCAGACAATGA 3806
Db 30203 CATGTTTCAANTAGCAGCGTGTGGCCCTCAACCCCTGCCACTTTCTCCAGAGATGG 30262
QY 3807 AGAAAAATARAAYATAAAGTGTCAACAARTAAATTTCTCAAACTATGCCACTCGAGGGGA 3866
Db 30263 GGAACCAATGACATGACTGCCCAACAAATATAGTCCAGACTATGCTCCCGAGATGA 30322
QY 3867 CTTTGTAGAGTTCCTTGTGATCTGATCCYAGCTTCAACTTGTATCTAGTGAAGTTCCT 3926
Db 30323 TCTCGTAGAGTCCCTTAACTAATCTGACCTT-AACCTATATCTAGTGAAGTTCAT 30381
QY 3927 TTTCTAGAAAAGGACTTTCGAAAAGYGGGTATGCAGTGGTCAGTGAATAATGGAATAVTTG 3986
Db 30382 TTTGGGAATGGATACGAGGCGAGTTACGCCATAGTTAGTGTAAACCATCTTG 30441
QY 3987 AAAGTAAATCCCTCACTCCAGGAAGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 4035
Db 30442 AAAGCAAGCTTACCAGAGACAGTCCAGTCCAGTGTAGTGAAGTGTAGT 30490

RESULT 12

US-08-979-847B-88

; Sequence 88, Application US/08979847B

; Patent No. 6582703

; GENERAL INFORMATION:

APPLICANT: PERRON, HERVE
BESEME, FREDERIC
BEDIN, FREDERIC
PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PEADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
TUBE, PHILIP

TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS

ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPH

THERAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIFF & BERRIDGE, PLC

STREET: P.O. BOX 19928

CITY: ALEXANDRIA

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/979,847B

FILING DATE: 26-No. 6582703-1997

CLASSIFICATION: <unknown>

ATTORNEY/AGENT INFORMATION:

NAME: BERRIDGE, WILLIAM P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 39046A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 703-836-6400

TELEFAX: 703-836-2787

INFORMATION FOR SEQ ID NO: 88:

SEQUENCE CHARACTERISTICS:

LENGTH: 2364 base pairs

TYPE: nucleotide

STRANDEDNESS: single

TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 88:

US-08-979-847B-88

Query Match									
Best Local Similarity 19.2%; Score 1452.4; DB 4; Length 2364;									
Matches 1813; Conservative 114; Mismatches 266; Indels 99; Gaps 18;									
QY	2021	ATGATCCAGCAGCAGGAGCTGAGGGTGCTGGGGCAAGGGCCATCCGATGCCATCACCTC	2080						
DB	1	ATGATCCAGCAGCAGGACGAGGGTGCCGGGGCAAGGGCCATCCGATGCCATCACCTC	60						
QY	2081	ACAGAGCCCTGGGTATGCTTGACCAATTGAGGGCCAGGAAGGT---TGTCCTCTGGACACT	2137						
DB	61	ACAGAGCCCCAGGTATGCTTGACCAATTGAGGGTCAAGAGGTNACTGTCTCTGGACACT	120						
QY	2138	GGTGGGTCTTCTTTAGTCTTACTCTTCTGTCGCGCAACACTGTCTCCAGATCTGTCACT	2197						
DB	121	GGCGNGCCTTCTCAGTCTTACTTTCCTGTCTGGCACAACTGTCTCCAGATCTGTCACT	180						
QY	2198	ATTCTGAGGGGTCCNTAAGACGGGCACTCACTAGATACCTTTTCCAGAGCACTAAGTTA	2257						
DB	181	GTCC--GAGGGGTCTTAGACAGCCAGTCACTAGATAC--TTCTCCAGAGCACTAAGTTG	236						
QY	2258	TGAACCTGGGAGCTTTATCTCTTTTCACATGCTTTTCTAAATTATGCTTTGAAGCCCACTA	2317						
DB	237	TG-ACTGGGAACTTTTACTCTTCCACATGCTTTTCTAAATTATGCTTGAAGGCCCACT	295						
QY	2318	CCTTGTTAGGGAGACATTTCTAGCAAAAGCAGGGGCCATTATACCTCGAACATAGGAG	2377						
DB	296	TCCTTGTGGGAGAGACATTTCTAGCAAAAGCAGGGGCCATTATACCTCGATATAGGAG	355						
QY	2378	AAGGAACACCCGTTTGTGTGTTGTCCTCTCTTGAGGAAGAAATTAATCTCGAAGTCTGGCA	2437						
DB	356	AAGGAACAACGTGTTGTGTGT-CCCTCTCTTGAGGAAGAAATTAATCTGAAGTCCGGCA	414						
QY	2438	ACAGAAGGCAATATGACACGAGCAAGAGATGCCGTCCTGTTCAAGTTTAAACTAAAGGA	2497						
DB	415	ACAGAAGGCAATATGAGCAAG-CAAGAAGATGCCCGTCTGTTCAAGTTTAAACTAAAGGA	473						
QY	2498	TTCCACTTCCCTTCCCTACCAAAAGGCAAGTACCCCTCAGACCCCAAGGCCCAACAAGGATT	2557						
DB	474	TTCCACTCTCTTCCCTACCAAGGCAAGTACCCCTCAGACCCGAGACCCCAAGGACT	533						
QY	2558	CAAAAAGATTGTTAAGGACTTAAAGCCCAAGGCTTAGTAAAAACCATGCATAACTCCCTG	2617						
DB	534	CAAAAAGATTGTTAAGGACCTTAAAGCCCAAGGCTAGTAAAAACCAAGCAATAGCCCTTG	593						
QY	2618	CAGTAATTCGTAGTGGAATTGAGGAGCAAGAAACCACTGACAGTGGAGGGTTAGTG	2677						
DB	594	CAAGACTCC-----AATTTTAGGAGTAGGAAGAACCAACGGACAGTGGG-GGTTAGTG	645						
QY	2678	CAAGACTCAGGATTATCAATGAGGCGGTGCTCTTTATACCCAGCTGTACTAGCCC	2737						
DB	646	CAAGAACTCAGGATTATCAAT-GAGGCTGTGTCTCTATACCCAGCTGTACTAACC	704						
QY	2738	TTATACTGTGMYTTTCCCAATACCAAGGAAGCAGAGTGCTTTTACASTCTCGACCTTMA	2797						
DB	705	TTATACAGTCTCTTTCCCAATACCAAGGAAGCAGAGTGCTTTTACAGTCTCGACCTTAA	764						
QY	2798	GGATGCGTCTTCTGCAATCCCTGTACATCTGACTCTCAATCTTGTGTCCTTTGAAGA	2857						
DB	765	GGATGCGCTTTTCTGCAATCCCTGTAGTCTGACTCTCAATCTTGTGTCCTTTGAAGA	824						
QY	2858	TACTTCAAAACCCARCATCTCAACTGAGGATTTTACCCCAAGGTTTCAAGGATAG	2917						
DB	825	TCCTTTGAACCCCAACGTCTCAACTCAGCTGACTGTTTATCCCAAGGTTTCAAGGATAG	884						
QY	2918	YCCCCACTATTTTGGCCAGGCATTTAGCCCAAGACTTGAGYCAATYMTACCTGACAC	2977						
DB	885	CCCCCACTATTTTGGCCAGGCATTTAGCCCAAGACTTGAGTCAATTCATCTGAGAC	944						
QY	2978	TCCTGTCTTCRGTAKGTGGATGATTACTTTTTTRGCGCCYRTRTCAGAAACCTTGTGCCA	3037						
DB	945	CTCTGTCTTCACTAGTATGATGATTACTTTTGTAGTCGCCGTTTCAAGAACCTTGTGCCA	1004						

Sequence 53, Application US/08979847B
Patent No. 6582703
GENERAL INFORMATION:
APPLICANT: PERRON, HERVE

BESEME, FREDERIC
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PARANHOS-BACCALA, GLAUCIA
KOMURIAN-PRADEL, FLORENCE
JOLIVET-REYNAUD, COLETTE
MANDRAND, BERNARD
GARSON, JEREMY
TUXE, PHILIP

TITLE OF INVENTION: VIRAL MATERIAL AND NUCLEOTIDE FRAGMENTS
ASSOCIATED WITH MULTIPLE SCLEROSIS, FOR DIAGNOSTIC, PROPHYL
THERAPEUTIC PURPOSES

NUMBER OF SEQUENCES: 210

CORRESPONDENCE ADDRESS:
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STREET: P.O. BOX 19928
CITY: ALEXANDRIA
STATE: VA
COUNTRY: USA
ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA: US/08/979,847B

APPLICATION NUMBER: US/08/979,847B
FILING DATE: 26-No. 6582703-1997
CLASSIFICATION: <Unknown>

ATTORNEY/AGENT INFORMATION:

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INFORMATION FOR SEQ ID NO: 53:

SEQUENCE CHARACTERISTICS:

LENGTH: 2391 base pairs

TYPE: nucleotide

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

SEQUENCE DESCRIPTION: SEQ ID NO: 53:

US-08-979-847B-53

Query Match 18.7%; Score 1415.8; DB 4; Length 2391;
Best Local Similarity 78.4%; Pred. No. 0;
Matches 1817; Conservative 109; Mismatches 267; Indels 126; Gaps 19;

Qy 2021 ATGATCCAGCAGCAGGATGAGGTCCTGGGGCAAGCCCATCCATGCCATCACCCCTC 2080

Db 1 ATGATCCAGCAGCAGGATGAGGTCCTGGGGCAAGCCCATCCATGCCATCACCCCTC 60

Qy 2081 ACAGAGCCCTGGGTATGCTTGACCAATGAGGGCCAGGAGGT---TGTCCTCTGGACACT 2137

Db 61 ACAGAGCCCTGGGTATGCTTGACCAATGAGGGTCAGAGGGGTNACTGTCCTCTGGACACT 120

Qy 2138 GGTGGGTCTTCTAGTCTTACTCTCTGTCCTGGGCAACACTGCTCTCCAGATCTGTCACT 2197

Db 121 GCGGNGCCTTCTAGTCTTACTTCTCTGTCCTGGGCAACACTGCTCTCCAGATCTGTCACT 180

Qy 2198 ATTCGAGGGGGTCCNTAAGCGGCGAGTCACATAGATATCTTTTCCAGCCACTAAGTTA 2257

Db 181 GTCC---GAGGGTCTTAGGACAGCCAGTCACTAGATAC-TTCCTCCAGCCACTAAGTTG 236

Qy 2258 TGAAGTGGGAGCTTTATCTTTTTCACATGCTTTTCTAATATGTTGTAAGAGCCCACTA 2317

Db 237 TG-AGTGGGAACTTTACTCTCTCCCATGCTTTTCTAATATGCTGCTGTAAGAGCCCACTC 295

2318 CCTTGTAGGAGAGACATCTTAGCAAAAGAGAGGGGCCATTATACACCTGAACATAGGAG 2377

Db TCTTGTGGGAGAGACATCTTAGCAAAAGAGAGGGGCCATTATACATGTGAATATAGGAG 355

Qy 2378 AAGGAACACCCGTTTGTGTGTCCTGCTTGAGGAAGGAATTAATCCTCAAGTCTCGGCA 2437

Db AAGGAACACCTGTTTGTGTGTCCTGCTTGAGGAAGGAATTAATCCTCAAGTCTCGGCA 414

Qy 2438 ACAGAGGACACATATGAGGAGGACCAAGAAATGCTGCTCTGTTCAAGTTAAATGAAGA 2497

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Qy 2498 TTCCACTCTCTTCCCTACCAAGGACGTACCCCTCAGAGCCCAAGGCCCAACAGGATT 2557

Db TTCCACTCTCTTCCCTACCAAGGACGTACCCCTCAGAGCCCAAGGCCCAACAGGATT 533

Qy 2558 CAAAAGATGTTAAGGACTTAAAGCCCAAGGCTTAGTAAACCATGATCACTCCCTG 2617

Db CAAAAGATGTTAAGGACTTAAAGCCCAAGGCTTAGTAAACCATGATCACTCCCTG 593

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Qy 2978 TCTTGTCTTCRGTAAGTGGATGATTTACTTTTGTGTCCTTTCAGAAAACCTTGTGCA 3037

Db TCTTGTCTTCRGTAAGTGGATGATTTACTTTTGTGTCCTTTCAGAAAACCTTGTGCA 1004

Qy 3038 TCAAGCCACCAAGCCTCTTTTAAATTTCTCGVACCTGTGCTACAGGTTTCCCAAGC 3097

Db TCAAGCCACCAAGCCTCTTTTAAATTTCTCGVACCTGTGCTACAGGTTTCCCAAGC 1064

Qy 3098 ARARGCTCARTCTGTCTCACAGCAGGTTAAATATCTTAGGCTAAATATTTCAAGGAC 3157

Db ARARGCTCARTCTGTCTCACAGCAGGTTAAATATCTTAGGCTAAATATTTCAAGGAC 1124

Qy 3158 CARGGCTCTCAGTGGAAATATCCAGCTTATCTGCTTATCTCTATCTCTCAAAACCT 3217

Db CARGGCTCTCAGTGGAAATATCCAGCTTATCTGCTTATCTCTATCTCTCAAAACCT 1184

Qy 3218 AAAGCAACTAAGGRRRTTCTTGGCTAAAGVGTCTGCGGCAAAATGATTTCCCAAGT 3277

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Db WTGCGCAATAGCCAGGCTATTAATATCAATTAAGGAACTCAGAAAAGCAATATCCC 1303

Qy 3338 ATTTATTAAGATGAGYATGAGYATGAGYATGAGYATGAGYATGAGYATGAGYATGAGY 3397

Db ATTTATTAAGATGAGYATGAGYATGAGYATGAGYATGAGYATGAGYATGAGYATGAGY 1358

Qy 3398 AACCCAGYCCAGTGTAAAGTGTGCGCAACRGGGCAAGACTTTTSTTTATATATACAGA 3457

[illegible]